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August 13, 2003, 15:21:20 ; Search time 47.9168 Seconds (without alignments) 2698.100 Million cell updates/sec
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1 MAPMLAALALLPVSEQG.......LFTIIATVAVLLSAPHIIVQ 501
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GenCore version 5.1.6 c. Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mcmnc:*
sp_ncganel:*
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sp_vertebrate:*
sp_unclassified:*

sp_plant:*
sp_rodent:*
sp_virus:*

sp_rvirus:*
sp_bacteriap:*
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SUMMARIES

Result		,					
	Score	Query	Query Match Length DB	DB	ID	Ď	Description
-	2640	100.0	501	5	09x2I4	50	09xzi4 heliothis v
7	2194	83.1	494	Ŋ	Q8T7S1	ŏ	08t7s1 drosophila
æ	2181	82.6	464	Ŋ	Q8T7S2	ğ	
4	2177	82.5	464	'n	Q8T7S3	ö	08t7s3 drosophila
5	2176.5	82.4	509	Ŋ	Q8T7S0	ő	08t7s0 drosophila
9	1156.5	81.7	523	Ŋ	O817R9	Ö	8t7r9 drosophila
7	1833	69.4	554	S	09VL79		09v179 drosophila
8	1803.5	68.3	496	Ŋ	09XZI3		9xzi3 heliothis v
9	1800.5	68.2	807	'n	O8T7V5	ő	8t7v5 drosophila
10	1786.5	67.7	545	Ŋ	61MA60	0	09vwi9 drosophila
11	1705.5	64.6	525	Ŋ	Q8IPE2	ő	Bipe2 drosophila
12 1	1258.5	47.7	502	11	9днр6		091hd6 mus musculu
13 1	1226.5	46.5	511	13	003481		003481 gallus gall
14 1	145.5	43.4	480	Ŋ	081932	0	81932 caenorhabdi
15	1132	42.9	461	'n	P91197	Ď,	P91197 caenorhabdi
16	1124	42.6	273	'n	91LV9Q	0	O9vit9 drosophila

O62083 caenorhabdi Q18556 caenorhabdi Q9nkdi drosophila Q8muro apis mellif Q46133 locusta miq	0.40	O9vc74 drosophila O96632 heliothis v O46128 heliothis v O8t0y9 aplysia cal		
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		ė.		(TrEMBLrel. 12, Last sequence update)	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	Putative nicotinic acetylcholine receptor alpha 7-2	Heliothis virescens (Noctuid moth) (Owlet moth).	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;						"Putative alpha subunits of insect nicotinic acetylcholine receptors	more similar to vertebrate alpha 7 subunits and C. elegans Ce21	to other insect nicotinic acetylcholine receptor alpha subunits.";	DBJ da	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.										Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;		56704 MW; 43CB0DC3960C78AB CRC64;	Score 2640; DB 5;	0;
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                                                                                       DVDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFD 120
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                        DEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP
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- SUBCELLIDIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
- I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

EMBL, AF321447; AAM13394.1;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
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Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE-21969411; PubMed=11973307;

Grauso M., Reenan M.A., Culetto E., Sattelle D.B.;

Grauso M., Reenan M. Carline Acetylcholine Receptor Subunit Genes,

"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify

Mediated Highly Conserved Target of Adenosine Deaminase Acting on R

Mediated A-to-1 Pre-mRAR Editing.";

Genetics 160:1519-1533(2002).
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda: Hexapoda; Insecta; Pterygota;
                                      Length 494;
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Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                              Indels
                                    ; Score 2194; DB 5;
; Pred. No. 5.7e-198;
31; Mismatches 37;
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FlyBase; FBgn0032151; nAcR-alpha-30D.
InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan_LBD.
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Q8T7S2;
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Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                                                                      494 AA;
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                                                                                                                                                                                                                                                                                           DLVLKDEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFF
                                                                                                                                                                                                                                                                                                                                                     356 TIMMNTRMRELELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNLGPGCSIFRTDFR
                                                                                                                                                                                                                                                                                                                                                                                                                                               RSFVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRF
                                                                                                                               Gaps
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Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Mediated A-to-I Pre-mRNA Editing.";
Genetics 160:1519-1533(2002).
                                                                                                                               20;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR GG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                         Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                        Length 494;
                                                                                                                               Indels
                                                                                494 AA; 56048 MW; 6EE711810EDE7BBB CRC64;
                                                                                                    ; Score 2181; DB 5;
; Pred. No. 9.6e-197;
35; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
          Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
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InterPro; IPR006029; Neu_channel_memb
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                                                                                                       82.6%;
81.6%;
                                                                                                                             Matches 413; Conservative
                                                                                                                  Local Similarity
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                                                                     Transmembrane
                                                                                SEQUENCE
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63 LQQIIDVDEKNQILTTNAWLNLEWNDYNLRWNETEYGGVKDLRITPNKLMKPDVLMYNSA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 DEGFDGTYHTNIVVKHNGSCLYVPPGIFKSTCKIDITWFPFDDQHCEMKFGSWTYDGNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 TIMMNTRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEGFDGTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 NLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGT
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type IV.
NACR-ALPHA-30D ON NACRALPHA-30D ON BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARI SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                         InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGRPAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
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FlyBase; FBgn0032151; nAcR-alpha-30D.
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MEDLINE=21969411; PubMed=11973307;
                                                                                                                                 InterPro; IPR006201; Neur_channel
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115

55 62

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RESULT 7
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Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Mediated A-to-I Pre-mRNA Editing.";
                                                                                                                                                                                                                                                                          Gaps
                                                        35;
                                                                                                                InterPro; IPR066201; Neur_channel.
InterPro; IPR066201; Neur_chan_LBD.
InterPro; IPR066202; Neur_chan_LBD.
InterPro; IPR06029; Neur_chan_LBD.
InterPro; IPR060292; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_memb; 1.
IGRRAMs; TIGR00860; LIC; 1.
BROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                   5; Length 509;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MRA-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-310D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit [1]).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                            509 AA; 57887 MW; BE8D8E0198E0C2BD CRC64;
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                                                                                                                                                                                                                                                 82.4%; Score 2176.5; DB 5;
80.2%; Pred. No. 2.7e-196;
ive 31; Mismatches 37;
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                                                                                                         FlyBase; FBgn0032151; nAcR-alpha-30D.
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Matches 418;
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123 DEGFDGTYHTIVVKHNGSCLYVPPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQL 182
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MEDLINE-21969411; PubMed-11973307;
Grauso M., Rechan R.A., Culetto E., Sattelle D.B.;
Grauso M., Rechan R.A., Culetto E., Sattelle D.B.;
Grauso Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drośophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Mediated A-to-1 Pre-mRNA Editing.";
Genetics 160:1519-1533(2002).
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 AA; 59110 MW; 1C200AF74F87F841 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.7%; Score 2156.5; DB 5; 77.6%; Pred. No. 2.1e-194; ive 32; Mismatches · 39;
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PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0032151; nACR-alpha-30D. InterPro; IPR006201; Neur_channel. InterPro; IPR006202; Neur_chan_LBD. InterPro; IPR006029; Neu_channel_memb. Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1. TIGRFAMS; TIGR00860; LIC; 1.
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01-MAY-2000 (TrEMBLrel. 13,
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                         Ephydroidea; Dro
NCBI_TaxID=7227
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Amanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,
R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R.A. Adams M.D., Celniker S.E., Lip P.W., Hoskins R.A., Galle R.F.,
R.A. George R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,
R.A. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,
R.A. Adams M. R.B. An H.-J., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basus A., Baxendale J., Bayraktaroglu L., Bassley E.M.,
Ballew R.M., Basus P.W., Barnen B.P., Bhandari D., Bolshakov S.,
R.A. Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
R.A. Charley S., Dahlke C., Davemport L.B., Davies P.,
R.A. Chander S., Dahlke C., Davemport L.B., Davies P.,
R.A. Cawley S., Dahlke C., Ferraz C., Ferriard S., Dunn P.,
R.A. Doub L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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R.A. Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.L.,
R.A. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
J. Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
J. Lasko P., Lel Y., Levitsky A.A., Li J., Ji Z., Liang Y., Lin Z.,
Lasko P., Lel Y., Levitsky A.A., Li J., Ji Z., Liang Y., Lin Z.,
Mount S.M., Moy M., Murphy B., Murphy L., Mozhref J.A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
Ralazzolo D.R., Relinfor K.A., Pobarry C., Morris J., Woshref R.A.
Rheifert K., Remington K., Saunders R.D., Shen H.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
R. Harley S., Wassarman D.A., Welsenbach J.,
Mullams S.M., Wooder Y., Wobarry C., Mu D., Yang S., Yao O., A.,
R. Harley R., Wassarman D.A., Welsenbach J.,
M. Harley R., Wassarman D.A., Welsenbach J.,
M. Harley R., Wester R., Wenter E., Wang A., Wang S., Yao O., A.,
R. Sheng K.H., Zhong F.N., Zhong Y., Zhu S., Zhu S., Zhon Q., Zheng L.,
Steince 287:2185-2195(2000).
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Celuiker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Carlson K., Dorsett V., Doup L.E., Dayle C., Dresnek D., Farfan D.,
Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
Amintosh T.C., Moy M., Murphy B., Neison C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richhards S., Scheeler F.,
Amillams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misra S., Crosh M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                        NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE-20196006; PubMed-10731132;
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                                                          S.E.;
                                                                                                                                                           S.E., Gibbs R.A., Rubin G.M., Venter C.J.; to the EMBL/GenBank/DDBJ databases.
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Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                             FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                             EMBL; AE003626; AAF52817.2; ...
FlyBase; FBGn003151; nacR-alpha-30D.
InterPro; IPR006201; Neur_channel.
InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONGHANNEL.
PROSITE; PS00336; NBENROTR_ION_CHANNEL; 1.
SEQUENCE 554 AA; 63236 MW; D6C63EB7F5B32A35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.4%; Score 1833; DB 5;
65.0%; Pred. No. 7.4e-164;
iive 36; Mismatches 67;
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Matches 370; Conservative
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                                                                                                                                                             Adams M.D., Celniker
Submitted (MAR-2000)
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 TRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVR 420
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 23, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
02-NAR-2003 (TrEMBLrel. 23, Last annotation update)
03-NAR-2003 (TrEMBLRel. 23, Last anno
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                                                                                                                                                                                                                                                                     27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496 AA; 56347 MW; 8032FED8515A6210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.3%; Score 1803.5; DB 5;
68.7%; Pred. No. 3.8e-161;
iive 53; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEVFTLFTIIATVAVLLSAPHIIV 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 68.7
Matches 347; Conservative
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI_TaxID=7102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLIS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LLALLPVSEQ----GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                          OR.
                                                                                                               01-JUN-2002 (TEMBLEE]. 21, Last sequence update)
01-MAR-2003 (TEMBLEE]. 23, Last annotation update)
10.MAR-2003 (TEMBLEE]. 23, Last annotation update)
10.MAC-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 oCG4498 OR CG16878.

Drosophila melanogaster (Fruit fly).

BLAIVIOTE; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota:
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TAXID=7227;
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InterPro; IPR006202; Neur_chan_LBD.
InterPro: IPR006029; Neur_chan_LBD.
InterPro: IPR006029; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
IGRRAMs; ITGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 68.2%; Score 1800.5; DB 5; 1 Similarity 66.3%; Pred. No. 1.5e-160; 348; Conservative 61; Mismatches 69;
                                 AA.
                                 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF272778; AAM13390.1; -.
FlyBase; FBgn0028875; nAcR-alpha-34E.
                                                                                             Created)
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                                                                                          01-JUN-2002
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Best Local 3
Q8T7V5
ID Q8T7V5
DT Q1-JUN--
DT O1-JUN--
DT O1-JUN--
DE NICOLID.
GN NGCK-ALI
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                                                                                                                                                                                                                                                                                                                                                                               Adams M.D. Celniker S. E., Holf R. A., Evans C. A., Gocayne J.D., RAM Amanatides P. G., Scherer S. E., Holf R. A., Hoskins R. A., Galle R.F., George R.A., Lewis S. E., Ii P. W., Hoskins R. A., Galle R.F., George R.A., Lewis S. E., Ii P. W., Hoskins R. A., Galle R.F., George R.A., Lewis S. E., Ii P. W., Hoskins R. A., Galle R. F., George R. A., Lewis S. E., I. I. P. W., Hoskins R. A., Galle R. D., Brandon R. C., Rogers Y. H. C., Blazel R. G., Champe M., Pfeiffer B. D., Man K. H., Doyle C., Baxter E. G., Helf G., Nelson C. R., Miklos G. L. G., Abril J. F., Agbayani A., An H. J., Andrews-Frankoch C., Balakov S. M. Ballew R. M., Basul A., Baxendale J., Barcktaroglu L., Beasley E. M., Ballew R. M., Backov B., Bouck J., Brokstein P., Borchter P. B., Borkova D., Botchen M. R., Bouck J., Brokstein P., Borchter P. S., Horkov S., M. Borkova D., Botchen M. R., Bouck J., Brokstein P., Brottler P., Burker S. A. Dowe D., Dew I. D., Dewis D., Dew I. D., Dew I. D., Dew I. D., Dewis D., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., McIncok J., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
                                                                                                                                                                                                                            Eutaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                          DEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHIIV
                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Last sequence upda 01-MR-2003 (TrEMBLrel. 23, Last annotation up CG32538 protein.

MARCA-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.

Drosophila melanogaster (Fruit fly).
                                                                                                                                                                 Created)
                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNGEWYLI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKNQLLITNIWLSLEW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 GPHEKRLLHALLDNYNSLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWEKLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 NDMNLRWNSSEFGGVRDLRIPPHRLWKPDVLMYNSADEGFDGTYATMVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 EKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 RTADIHEMPOWIKSVFLOWLPWILRMSRPGK------KITRKTIMMNTRMRELEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VGGGL-----GSHHRELHLILRELQFITARMKKADEEAELISDWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                      Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E.; Smith C.D., Tupy J.L., Berqman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris h Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003511; AAF48950.2; -
FlyBase; FB90031014; nAcR*alpha-18C.
FlyBase; FB9006201; Neur_chan=1.
InterPro; IPR006201; Neur_chan=1.EBD.
InterPro; IPR006202; Neur_chan=1.EBD.
InterPro; IPR006029; Neur_chan=1.EBD.
InterPro; IPR006029; Neur_chan=1.EBD.
InterPro; IPR006029; Neur_chan=1.
Ffam; PF02931; Neur_chan_memb. 1.
Pfam; PF02932; Neur_chan_memb. 1.
FTGRAMS; TIGR00806; LIC; I.
FROSIPE; PS00236; NEUROTR_LON_CHANNEL; 1.
FROSIPE; PS00236; NEUROTR_LON_CHANNEL; 1.
SEQUENCE 545 AA; 61517 MW; 7B83025107A66209 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.7%; Score 1786.5; DB 5; 66.7%; Pred. No. 1.8e-159; ive 56; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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RX MEDLINE-20196006; Pubbled-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides F.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,

Sutton G.G., Northan J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Regers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Renos P.V., Bernan B.P., Blandari D., Botahakov S.,

Berkova D., Botchan M.R., Baude H., Cadeu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,

RA Goon R., Doup L.E., Downes M. Dugan Rocha S., Plunkov B.C., Dunn P.,

RA Burtis R.J., Harvey D., Helman T.J., Hernandez J.R., Rotckinan W.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Rotcky D., Halman T.J., Hernandez J.R., Ketchum K.A.,

Jalali M., Kalush F., Karpen G.H., Kazit C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntoon T.C., Morris J., Mosherson D.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Mizny D.M., Nelson D.L.,

Rainer K., Remington K.A., Howlen R., Stropki M.P., Santh T.,

Rainer K., Remington R., Saunders R.D., Stropki M.P., Santh T.,

Rainer K., Remington R., Saunders R.D., Stropki M.P., Santh T.,

Ray Spier E., Ston-Klamos I., Simpson M., Stropki M.P., Santh T.,

Ray Shie R., Tector C., Turner R., Venter E., Wang S., Yao O.,

RA Willams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao O.,

RA Shies R., Tector C., Turner R., Venter E., Wang S., Yao O.,

RA Shies R., Zhon M., When S., Whyers E.W., Wallson D.K.,

Ray Shies S., Labor M., Shang G., Labor C., Siden-Klamos I. Simpson M., Strong S., Sun E.,

Ray Shies S., Jenger B.W., Rub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Barzon J., An H., Baldwin D., Barzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galler R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,
MINITOSH T.C., MOY M., Murphy B., Welson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                             01-WAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
  FAAMVVDRFCLFVFTLFTIATVAVLLSAPHIIV
                        525 AA.
                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:2185-2195(2000).
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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467
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432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLVLKDEAGGDLSDFITNGEWYLIGM-PGKKNTITYACCP-------EPYVDVT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 -----ILFFQFNCAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKPCRRVH 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLPASLSLFVLLIFLAIIKESCQCPHEKRLINHLLSTYNTLERPVANESEPLEVKFGLT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 CNHKDLHLILKELQFITARMRKADDEAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 -----TILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 ADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQC-RAESTYFNCIMFMVASSVVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 VVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMRELELKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 SKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVRPSTMEDVGGGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 SKSLLANVLDIDDDFRH-----TISGSQTAIGSS-----ASFGRPTTVEEHHTAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 APMLAALAL-----LALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                      Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Sarle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                  Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 FTIMIRRRTLYYFFNLIVPCVLISSMALL----GFTLPPDSGEKLTLGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.6%; Score 1705.5; DB 5; Length
63.2%; Pred. No. 7.3e-152;
Live 43; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AE003626; AAN10709.1; - SEQUENCE 525 AA; 60135 MW; CF95283C56EA90A9 CRC64;
                                                                                                                                                                                                                                                                                       Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                             (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 63.2 nes 347; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSAPHIIVQ 501
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                                                                                                       SEQUENCE FROM N. A.
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RESULT 12 Q9JHD6

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305 ASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMR 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF0231; Neur_chan_LBD; 1.
Pfam; PF0231; Neur_chan_memb; 1.
Pfam; PF0232; Neur_chan_memb; 1.
TIGRPAM; TG7600860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
                                                            478 FVFTLFTIIATVAVLLSAPHII 499
                                                                            473 MAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90315158; PubMed-2369519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 PA
58705 MW;
                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel, 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 46.6%
Matches 246; Conservative
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 AA;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 ASVELSAGAGPPSSNGNLLXI--GFRGLEGMHCAPTPDSGVVCGRL--ACSPTHDEHLMH 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAL-LALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELKERSS - - - - KSLLANVLDIDDDFR - - - - +GPPPPPNSTASTGNLGPGCSIFRTDFRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
MGD; MGI:99779; Chrna7.
                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                             Stitzel J.A., Farnham D.A., Collins A.C.;
"Linkage of strain-specific nicotinic receptor alpha 7 subunit restriction fragment length polymorphisms with levels of alphabungarotoxin binding in brain.";
Brain Res. Mol. Brain Res. 43:30-40(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.7%; Score 1258.5; DB 11; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.8%; Pred. No. 9.6e-110;
tive 77; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 AA; 56617 MW; C9353E5136D620E3 CRC64;
                                            01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Nicotinic acetylcholine receptor subunit alpha 7.
502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00236; NEUROTR_ION_CHANNEL; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neu_channel_memb.
                              Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                               MEDLINE=97189245; PubMed=9037516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 49.8 nes 250; Conservative
PRELIMINARY;
                            (TrEMBLrel.
                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGR00860;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                       STRAIN-DBA/21bg;
                                                                                                                                                                                                 STRAIN-DBA/21bg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
                           01-OCT-2000 (
01-OCT-2000 (
01-MAR-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75
418 FVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCL
                                   423 GTHPSDGDP------DLAKILEEVRYIANRFRCQDESEVICSEWKFAACVVDRLCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 LWASLFLSFFKVSQQGESQRRLYRDLLRNYNRLERPVMNDSQPIVVELQLSLLQIDDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23) Last annotation update)
Alpha8 subunit of nicotinic acetylcholine receptor precursor.
Gallus gallus (Chikken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 GDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily ";

Neuron 5:35-48(1990)

-1-SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-1-STMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

EMBL; X52996; CAA36544.1;

InterPro; IPR006201; Neur_channel.

InterPro; IPR006202; Neur_channel.

InterPro; IPR006202; Neur_channel.memb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.; "Brain alpha-bungarotoxin-binding protein cDNAs and mABs reveal subtypes of this branch of the ligand-gated ion channel gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
10F362D153EC87A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1e-106
                                                                                                                                                                                                                                                                                                                                              511 AA.
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MFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTI--M 358
                                                                                                       359 MNTRMRELELKERSSKSLLANVLD-----IDDDFRHGPPPPNSTASTGNLGPGCS .408
                                                                                                                                                                 IFRTDFRRSFVRPSTMEDVGGGLGSHHRE-----LHLILRELQFITARMKKADEEAELIS 463
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.9%; Score 1132; DB 5; Length 4 44.7%; Pred. No. 7.2e-98; ive 86; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Gattung S., Maggi L.;
"The sequence of C. elegans cosmid D2092.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane; Transmembrane.
1 AA; 52718 MW; 6182A7F827357B92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Glycoprotein; Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U88167; AAB4223.1; ...
Wormbep; D2092.3; CE09102.
InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_channel.
InterPro; IPR0060202; Neur_channel.memb.
Pfam; PF02931; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_memb; 1.
PRINTS; PR00252; NRIOKHANTEL.
PIGREAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL,
                                                                                                                                                                                                                                                                                                                                  461
                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN*Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Cree 01-MAY-1997 (TrEMBLrel. 03, Last 01-MAR-2003 (TrEMBLrel. 23, Last Hypothetical 52.7 kDa protein. 20092.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.7
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                          471
                                                                                                                                                                                                                                           Waterston R.;
"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                            DWKFAAMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
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                                                                                                                                                                  409
                                              301
                                                                                                                                      360
                                                                                                                                                                                              413
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                                                                                                                          | |------PQN-NDLGSKSGKITCPLSEDNEHVQKKALMDTIPVIVKILEEVQFIAMR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELELK-----ERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL------GPGCSIF 410
                                                                                                         -----SHHRELHL------ILRELQFITAR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 VDEKNQVYYVNAWLDYTWNDYNLVWDKAEYGNITDVRFPAGKIWKPDVLLYNSVDTNFDS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAGG-DLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300
                 ------ X 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis
                                                                          362 PLSCKYSYPKHHPSLKNTEMNVL------PGHQPSNGNMIYSYHTMENPCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 480;
                                                                                                                                                                                  FRKQDEGEEICSEWKFAAAVIDRLCLVAFTLFAIICTFTILMSAPNFI 503
                                                                                                                                                                  452 MKKADEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
Nelson J., Wohldmann P.;
"The sequence of C. elegans cosmid F25G6.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases: AF022973; AAN84815.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55274 MW; B5D6B707E50228A3 CRC64;
                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
1 MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acctylcholine receptor protein 16, 1soform b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 43.4%; Score 1145.5; DB 5; Best Local Similarity 47.3%; Pred. No. 4.1e-99; Matches 231; Conservative 71; Mismatches 135;
                                                                                                                                                                                                                                                                        480 AA.
                                                                                                       411 RIDFRRSFVRPSTMEDVGGGLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.;
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                                                                                                                                                                                              456
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                                                                                                                                     407
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                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                         081932
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Search completed: August 13, 2003, 15:29:11 Job time : 49.9168 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 13, 2003, 15:14:55; Search time 10.4907 Seconds (without alignments) 2245.843 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-303-232-6 2640 1 MAPMLAALALLPVSEQG......LFTIIATVAVLLSAPHIIVQ 501

Scoring table:

127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:.

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P36544 homo sapien	2 mus m	_	Q05941 rattus norv	_	30 caen	(D)	_	Q07263 bos taurus	P09478 drosophila			P23414 schistocerc	P17644 drosophila			Q15822 homo sapien		rattus	P49581 gallus gall	rattus		-	σ	P04755 drosophila	rattn	1 homo sa	79 gallu		32 gallu	08 rattus	6153 gallu	P30926 homo sapien
COTTON		. OI	ACH7_HUMAN	ACH7_MOUSE	ACH7_CHICK	ACH7_RAT	ACH7_BOVIN	ACH1_CAEEL	ACH3_HUMAN	ACH3_RAT	ACH3_BOVIN	ACH1_DROME	ACH3_CHICK	ACH1_MANSE	ACH1_SCHGR	ACH2_DROME	ACH6_HUMAN	ACH2_CHICK	ACH2_HUMAN	ACH3_CARAU	ACH2_RAT	ACH6_CHICK	ACH6_RAT	ACHP_RAT	ACH4_DROME	ACHA_BOVIN	ACH3_DROME	ACHN_RAT	ACH4_HUMAN	ACHA_CHICK	ACHN_HUMAN	ACH4_CHICK	ACHA_RAT	ACHP_CHICK	ACHP_HUMAN
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ALIGNMENTS

ACHT_HUMAN STANDARD; PR554; 015826; 096RH2; 09555; 09BXH P85544; 015826; 096RH2; 09555; 09BXH 01-NOV-1997 (Rel. 29, Created) 01-NOV-1997 (Rel. 35, Last sequence user-EB=2003 (Rel. 41, Last annotation Neuronal acetylcholine receptor prote CHRNA7 OR NACHRA7. HOMO sapiens (Human). EUKARYOGA: Metazoa; Chordata; Craniat Mammalia; Eutheria; Primates; Catarrh NCBI_TAXID=9606; [1] SEQUENCE FROM N.A. TISSUE=Brain A acetylcholine receptor from the SH-9528; Peng X., Katz M., Gerzanich V., Anand Properties of native receptors and fuexpressed in Xenopus cocytes."; Mol. Pharmacol. 45:546-554(1994). [2] ELIDOTE FROM N.A. TISSUE=Hippocampus; Logel J., Drebing C., Barnhart M., An SEQUENCE FROM N.A. TISSUE=Hippocampus; Logel J., Drebing C., Barnhart M., An Submitted (DEC-1995) to the EMBL/GenB [3] ELIDOTE A Incotinic acetylcholine receptorative structure of human neuro comparative structure of human neu		
	AC D	ACH7_HUMAN STANDARD; PRT; 502 AA. P36544; Q15826; Q96RH2; Q99555; Q9BXH0;
	T C	01-JUN-1994 (Rel. 29, Created)
	5 5	or-nov-1997 (Ref. 35, Last sequence upwate) 28-FEB-2003 (Rel. 41, Last annotation update)
	DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
	SO	Homo sapiens (Human).
•	20	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	2 6	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
•	N N	NCB1_IGXID=9000;
·	RP	SEQUENCE FROM N.A.
·	2 2	
	¥ 6	MEDLINE=94190263; VUDMed=6140/36; Dona V Vatr M Corrector N Name D Tindeton I.
	Z Z	Felig A., Natz M., Gelzanich V., Ahana K., Lindstrom J.; "Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subuni
	RŢ	from the SH-SY5Y cell line and determination of pharmacological
	RT	properties of native receptors and functional alpha 7 homomers
•	E E	expressed in Xenopus oocytes."; Wol pharmacol 45.546-554/1994)
·	R'N	[2]
•	RP	SEQUENCE FROM N.A.
•	S 5	TISSUE-Hippocampus;
•	A P	LOGEL J., Drebing C., Barnnart M., Antle C., Leonard S.; Submitted (DRC-1995) to the EMBL/GenBack/Ond. databases
·	RN	[3]
•	RP	SEQUENCE FROM N.A.
•	X 5	MEDLINE=97062879; PubMed=8906617;
	R A	Chavez-Noriega I. E. Johnson E. C. Velicelebi G. Harnold M.M.
•	RT	"Comparative structure of human neuronal alpha 2-alpha 7 and beta
	RT	2-beta 4 nicotinic acetylcholine receptor subunits and functional
	RT	expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
•	E I	Deta 4 Subunits."; J Mol Neurosci 7:217-228/1996/
•	RN	(4)
	КР	SEQUENCE FROM N.A.
•	ž	MEDLINE=97162233; PubMed=9009220;
•	X E	GIOGE NOTHELLIN F.J., LUYLEH W.H.M.L.; "Cloning and segmence of full-length chins encoding the himan neuron
•	RT	nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 an
	$\mathbf{R}\mathbf{T}$	expression of seven nAChR subunits in the human neuroblastoma cell
•	RT	line SH-SY5Y and/or IMR-32.";
	A W	FEBS Lett. 400:309-314(1997). [5]
	RP	REVISIONS.
	RA	Groot Kormelink P.J., Luyten W.H.M.L.;
	R.	Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
	RP	SEOUTENCE FROM N.A.
	2	TISSUE=Epidermal keratinocytes;
	RA	Arredondo J., Grando S.A.;

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ACH7_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .; TAS.
                                                                                                                                                                                                                      *Molecular cloning and chromosomal localization of the human alpha 7-nicotinic receptor subunit gene (CHRNA7).";
                                                                                                                                                                                                                                                                                          MEDIINE-21818878; PubMed-11829490; Riley B., Williamson M., Collier D., Wilkie H., Makoff A.; "A 3-Mb map of a large segmental duplication overlapping the alpha7-nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14."; Genomics 79:197-209(2002).
                                                                                                                                                                                                                                                                                                                                                                                                             MEDITE-21829512; University Pubmed=11840567; Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A., Parentis R.A., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J., Zvelebil M.J., Page M.J., "Cluster analysis of an extensive human breast cancer cell line protein expression map database."; Proteomics 2:212-223(2002).

-!- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                          Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
MASS SPECTROMETRY: WW-54157.68; METHOD=MALDI.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                     Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti M., Helnemann S.F.;
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GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan.
GO; GO:0006889; F:nicotinic acetylcholine-activated cation-se.
GO; GO:0006889; F:nicotinic of MAPK; TAS.
GO; GO:0006812; P:small molecule transport; TAS.
InterPro; IPR006029; Neu_channel_nemb.
InterPro; IPR006202; Neu_channel.
InterPro; IPR006201; Neu_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEMBRANE.
SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
                                                                     Lee J., Tian J., Giordano T.;
Cloning and sequence of the human a7 nicotinic acetylcholine
 Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC
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                                                                                                                                                                               MEDLINE-94245214; PubMed-8188270;
                                                                                                                    Drug Dev. Res. 30:252-256(1993).
                                                                                                                                                                                                                                                                                  SEQUENCE OF 118-129 FROM N.A.
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X08420; CAA69697.1; -.
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PIR; G02259; G02259.
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Genew; HGNC:1960; CHRNA7.
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ASSOCIATED WITH RECEPTOR ACTIVATION
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          Pfam; PF02932; Neur_chan_memb; 1.
PRINTS: PR00252; NRICONCHANNEL.
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PROSITE: PS00265; NEUROTR_ION_CHANNEL; 1.
POSTSYNAPTIC membrane; Ionic channel; Glycoprotein; Signal;
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48.6%; Pred. No. 1.4e-103;
tive 75; Mismatches 138;
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                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BÝ SIMILARITY.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                      acetylcholine receptor.";
Genomics 26:399-402(1995)
-!- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
C9312E5260120E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                              SUBCECLULARIA LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-CATED IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                           SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 502;
                                                                                                                                                                               STRAIN-BALB/C; TISSUE-Brain;
MEDILE-95324936; PubMed-7601470;
Orr-Urtreger A., Saldin M.F., Baldini A., Beaudet A.L.;
"Cloning and mapping of the mouse alpha 7-neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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49.6%; Pred. No. 2.5e-103;
tive 78; Mismatches 148;
  502 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A57175; A57175.
MGD; MGI:99779; Chrna7.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD.
Pram; PF02931; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
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56631 MW;
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  STANDARD;
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502 AA;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                          NCBI_TaxID=10090;
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                                                                                 CHRNA7 OR ACRA7
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SIGNAL
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                                                                                                 musculus
ACH7_MOUSE
P49582;
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CARBOHYD
SEQUENCE
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306 417 422 477 246 127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186 MALLGFTLPPDSGEKLTLGVT1LLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306 SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366 366 367 ASVELSAGAGPPTSNGNLLYI --GFRGLEGMHCAPTPDSGVVCGRL--ACSPTHDEHLMH LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS ELKERSS----KSLLANVLDIDDDFR-----HGPPPPNSTASTGNLGPGCSIFRTDFRRS 418 FVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCL Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S., Millar N., Valera S., Barkas T., Ballivet M.; Partra T., Ballivet M., Partra T., Ballivet M., Balli T., Bal **OLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN** Gallus gallus (Chicken). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; 01-Aug-1991 (Rel. 19, Created)
1-Aug-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor. and MAbs reveal SEQUENCE OF 1-18 FROM N.A. STRARIF=White leghorn; TISSUE=Erythrocyte; MEDILNE-97049204; Pubbed-145587; MATLET-SAGZINSKI L., Hernandez M.C., Roztocil T., Ballivet M., Lindstroem J.; Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstroem J. Brain alpha-bungarotoxin binding protein cDNAs and MADS revesubtypes of this branch of the ligand-gated ion channel gene superfamily."; 502 AA. 478 FVFTLFTIIATVAVLLSAPHII 499 PRT; TISSUE=Brain; MEDLINE=91097796; PubMed=1702646; MEDLINE-90315158; PubMed-2369519; STANDARD; by alpha-BTX."; Neuron 5:847-856(1990). Neuron 5:35-48(1990). SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI_TaxID=9031; TISSUE=Brain; ACH7_CHICK P22770; 67 20 187 187 247 307 307 367

Matter J.M.;

99

Gaps

27;

Indels

Matches

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Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor. 
promoter develops during morphogenesis of the central nervous
                                                                                                                                                       Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A., Ray N., Raftery M.A.; "Brain and muscle nicotinic acetylcholine receptors are different but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                         MEDLINE-92049732; PubMed-1719423; Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C., Hussy N., Bertrand S., Ballivet M., Changeux J.-P.; P.: "Mutations in the channel domain alter desensitization of a neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- DEVELOPMENTAL STRAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
MEDLINE=93024917; PubMed=1383829;
Galazi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
Changeux J.-P., Bertrand D.;
Mutations in the channel domain of a neuronal nicotinic receptor
convert ion selectivity from cationic to anionic.";
Nature 359:500-505(1992).
I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANCE IN CONFORMATION THAT AFFECTS ALL SUBJUITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHABUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
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                                                                                                                                                                                                                  homologous proteins.";
Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Multigene family; 3D\text{-structure}. SIGNAL 1 23
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                   TISSUE=Brain;
MEDLINE=85270494; PubMed=3860855;
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PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGRO0860; LIC; 1.
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Pfam; PF02932; Neur_chan_memb; 1
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EMBL; X68246; CAA48317.1; -.
EMBL; X6856; CAA48576.1; -.
PIR; JN0113; JN0113.
PDB; IKC4; 17-APR-02.
PDB; IKL8; 17-APR-02.
                                                          EMBO J. 11:4529-4538(1992)
                                                                                                                                                                                                                                                                                                                                                                          nicotinic receptor.";
Nature 353:846-849(1991).
                                                                                                                                                                                                                                                                           MUTAGENESIS OF LEU-270.
                                                                                                 SEQUENCE OF 24-47.
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                                                                                                                                                                                                                                                                                                                                                                                                                       125 TEHTNYLVNSSGHCQYLPPGIFKSSCYIDVRMFPFDVQKCNLKFGSWTYGGWSLDLQMQE 184
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                                                                                                                                                                                                                                                                                                                                  62 VDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG 121
                                                                                                                                                                                                                                                                                                                                                                                                   122 TYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 FMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNT 361
                                                                                                                                                                                                                                                                   2 APMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIID
                                                                                                                                                                                                                                                                                   182 EAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
MEDLINE-93147931; PubMed=7678857;
Sequela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
"Molecular cloning, functional properties, and distribution of rat brain alpha 7: a nicotinic cation channel highly permeable to
                                                (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
L-SA, T. SUPPRESSES INHIBITION BY THE
OPEN CHANNEL BLOCKER (DX-222.
OR -> ET (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1998 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
CHRNA7 OR ACRA7.
                                ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                 47.5%; Score 1253; DB 1; Length 502; 48.8%; Pred. No. 4.2e-103;
                                                                                                                                                                                                                                  81; Mismatches 145; Indels
                                                                                                                                                                  572325D4309AD2FD CRC64;
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                                                                                                                                                                      56946 MW;
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Best Local Similarity 48.89
Matches 250; Conservative
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502 AA;
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 TRANSMEM
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P54131;
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                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAL-LALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                       mitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. EVUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                    SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGANN-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                  R EMBL, L31619; AAC33136.1; --
R PIR; T01378; T01378.
R InterPro; IPR006020; Neur_channel_memb.
R InterPro; IPR006202; Neur_channel.
R InterPro; IPR006201; Neur_channel.
R Pfam; PF02931; Neur_chan_memb; 1.
R PRIME; PR02932; NRUCCHANNEL.
R PRIME; PS00236; NEUROTR_ION_CHANNEL; 1.
R PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
R PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
R POSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
R POSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
R POSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
R SIGNAL
                                                                                                                                                                               SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78; Mismatches 149; Indels
                                                                   Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-7 CHAIN. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00996E74EC7B9A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N -> F (IN REF. 2).
P -> R (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.2%; Score 1246.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                  STRAIN-Sprague-Dawley; TISSUE-Brain;
                                             STRAIN=Sprague-Dawley; TISSUE=Brain;
          Neurosci. 13:596-604(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56410 MW;
                                                                                                                                                                                                                                                                                                                                         EMBL; S53987; AAB25224.2; -.
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490
164
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90
133
447
469
502 AA;
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                                  SEQUENCE FROM N.A.
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231
262
296
318
470
150
                                                                                        REVISION TO
                                                                                                               Hartley M.;
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DISULFID
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CONFLICT
SEQUENCE
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  calcium.'
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                                    247 LALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
                                                                                                                                                                                                                                                                                                                                                                                                                          366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
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VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                       LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
                                                                                                                                                                            MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELKERSS----KSLLANVLDIDDDFR----HGPPPPNSTASTGNLGPGCSIFRTDFRRS
                                                                                                                                                                                                                                                                                                                                                                                                                          SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
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Eur. J. Neurosci. 7:647-655(1995).

-!- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CORPORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-1996 (Rel. 34, Created)
1-0cT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOId=P54131-2; Sequence=VSP_000075;
TISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS.
SIMILARITY: BELONGS TO THE LIGAND-GATED TONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95346009; PubMed-7620615;
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 AA.
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473 MAFSVFTIICTIGILMSAPNFV 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELKERSS----KSLLANVLDIDD---DFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFV 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCLFV 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALLGFTLPPDSGEKLTLGVT1LLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                                                                                                       NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                        ASSCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MISSING (In isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 499;
                                                                                                                                                                                       PIGNITS; PRO255; NUTRINGEL.
TIGREAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_LON_CHANNEL; 1.
PROSITE; PS00236; NEUROTR_LON_CHANNEL; 1.
Transmembrane; Multigene family; Alternative splicing.
Transmembrane; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
47.0%; Score 1240.5; DB 1; Length
Best Local Similarity 49.4%; Pred. No. 5.3e-102;
Matches 247; Conservative 78; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEE5D0B3820D42D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                        InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neu_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
Ffam; PF02931; Neur_chan_LBD; I.
Pfam; PF02932; Neur_chan_memb; 1.
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                                                                                                                EMBL; X93604; CAA63802.1;
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161
210
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CARBOHYD
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditís.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96196478; PubMed-8627624;
Ballivet M., Alliod C., Bertrand S., Bertrand D.;
"Nicotinic acetylcholine receptors in the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACETYLCHÓILNE RECEPTOR LIKE PROTEIN.
ALPHA-TYPE CHAIN.
EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                             LO FED-ZUUJ (REL. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor.
F25G6.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TICRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
Nelson J., Wohldmann P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                     498 AA
                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; F2566.3; CE09639.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_memb; 1.
PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                       PRT;
480 FTLFTIIATVAVLLSAPHII 499
                              472 FSVFTILCTIGILMSAPNEV 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Mol. Biol. 258:261-269(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X83887; CAA58764.1; -.
EMBL; SAP022973; AAC25796.1; -
PIR; SG8588; SG8588.
HSSP; PS8154; 1198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314
472
493
161
212
                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
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498
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93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                       ACH1_CAEEL
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CARBOHYD
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TRANSMEM
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                                                                                                                                                                                                                                                                                           IFRTDFRRSFVRPSTMEDVGGGLGSHHRE-----LHLILRELQFITARMKKADEEAELIS 463
                                                                                                                                                                                                                                                                                                      61
                                                                   61
                                                           VDEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG
                                                                                                                                                      EAGG-DLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP
                                                                                                                                                                                       CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI
                                                                                                                                                                                                                        301 MFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTI--M
                                                  2 APMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIID
                                                                                                                                                                                                                                                          359 MNTRMRELELKERSSKSLLANVLD-----IDDDFRHGPPPPNSTASTGNLGPGCS
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coding for the alpha 3 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                       ACH3.HUMAN STANDARD;
973.297, 0158.023, 0956.035, 0995.035, 0990.035, 001.0CT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
CHRNA3 OR NACHRA3.
                                  51;
                 Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90245396; PubMed-2336208; Fornasari D., Chini B., Tarroni P., Clementi F.; Molecular, cloning of human neuronal nicotinic receptor alpha
                                  Indels
E463ABB40AC9FA82 CRC64;
                                                                                                                                                                                                                                                                                                                             DWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                                                                                                                                                     140;
               Score 1237.5; DB 1
Pred. No. 9.7e-102;
                                 80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mihovilovic M., Roses A.D.;
"Expression of mRNAs in human thymus of a neuronal acetylcholine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of a neuronal acetylcholine receptor
Exp. Neurol. 111:175-180(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurosci. Lett. 111:351-356(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91114756; PubMed=1989896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A. (ISOFORM 1).
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SEQUENCE FROM N.A. (ISOFORM 2)
57169 MW;
                                  245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
498 AA;
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-subunit.
SEQUENCE
                                                                                   62
                                                                                                                     122
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                         Best Local
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Both M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garria A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chenerth A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.; "The structures of the human neuronal nicotinic acetylcholine receptor beta2- and alpha3-subunit genes (CHRNB2 and CHRNA3)."; Hum. Genet. 103:645-653(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human neuronal and beta4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECTENCE FROM N.A., AND VARIANT LEU-21 INS.
MEDLINE-21342809; Pubmed-11450844;
Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
"Characterization of the human beta4 nAChR gene and polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE
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"Cloning cholinergic receptors in human keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER BINDING. THE RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE-27162233; PubMed-9009220;

Groot Kormelink P.J., Luyten W.H.M.L.;

"Cloning and sequence of full-length cDNAs encoding the human neuro micoflinic acetylcholine receptor (nAchR) subunits beta3 and beta4 and expression of seven nAchR subunits in the human neuroblastoma cell ine SH-SYSY and/or IMR-32.";
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A., Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.; "Comparative structure of human neuronal alpha 2-alpha 7 and beta expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anand R., Lindstrom J.; Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TO SUBUNITS: ALPHA AND NON-ALPHA (BETA).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                  beta 4 subunits.;
J. Mol. Neurosci. 7:217-228(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE-99118870; PubMed-9921897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Genet. 46:362-366(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Epidermal keratinocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS Lett. 400:309-314(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
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Gaps

61;

Indels

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131 VDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTWKFGSWSYDKAKIDLVLI 190
                                                                                                              DVDEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFD 120
                                                                                                                                                      GTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLK 180
                                                                                                                                                                                                181 DEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP 240
                                                                                                                                                                                                                                        241 CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300
                                                                                                                                                                                                                                                    301 MFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMN 360
                                                                                                                                                                                                                                                                                                                                                                                396 QDGMCGYCHHRRIKISNFSANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMKA 455
                                                                                                                                                                                                                                                                                                                         361 TRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL-----GPGCS---- 408
                                                                                                                                                                                                                                                                                                                                            -----TSNEGNAQKPRPLYGAELSNLNCFSRAESKGCKEGYPC 395
                                                                                                                                                                                                                                                                                                                                                                  -----IFRIDFRRSFVRPSTMEDVGG--GLGSHHRELHLILRELQFITARMKK 454
                                                                     1 MAPMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII 60
                                                                                 DB 1; Length 503;
L -> V (IN REF. 1).
8A9EBC5D71AEC7D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         455 ADEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLL 493
                            ; Score 989.5; DB 1;
; Pred. No. 9.2e-80;
92; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
        57309 MW;
                              37.58;
                                       38.58;
                                         Best Local Similarity 38.59
Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
         503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACH3_RAT
P04757;
                                                                                                                61
                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                   409
         SEQUENCE
 CONFLICT
                             Query Match
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                  IsoId=P32297-2; Sequence=VSP_000073;
Note=No experimental confirmation available;
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
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MALAV -> MGSGPL (in isoform 2).
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LSPP -> CRA (IN REF. 1).
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EXTRACELLULAR (POTENTIAL)
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D -> G (IN REF. 1).
DD -> TT (IN REF. 1).
I -> S (IN REF. 1).
          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP_000073.
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                              IsoId-P32297-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
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EMBL, U62432, AAB40110.1; -
EMBL, V08418, CAA6595.1; -
EMBL, AJ007783, CAA07682.1; -
EMBL, AJ007784, CAA07682.1; JOINED.
EMBL, AJ007785, CAA07682.1; JOINED.
EMBL, AJ007785, CAA07682.1; JOINED.
EMBL, AJ007787, CAA07682.1; JOINED.
EMBL, BC001642; AAH01642.1; JOINED.
                                                                                                                                                                                                                                                                                 EMBL; BC002996; AAH02996.1; -. EMBL; BC000513; AAH00513.1; -.
                                                                                                                                                                                                                                                                                                     EMBL; AF385584; AAK68110.1; -.
                                                                                                                                                                            EMBL; M86383; AAC84176.1; -.
                                                                                                                                                                                                                                                                                                               EMBL; X53559; CAA37625.1;
                                                                                                                                                                                                                                                                                                                                   PIR; A53956; A53956.
Genew; HGNC:1957; CHRNA3.
 ALTERNATIVE PRODUCTS:
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289
326
475
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PIR; A53956; A53956.
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SEQUENCE FROM N.A.
MEDLINE-88041184; PubMed-2444984;
Boulter J., Connolly J.G., Deneris E.S., Goldman D.J., Heinemann S.F.,
Patrick J.;
"Functional expression of two neuronal nicotinic acetylcholine
"Functional expression of two neuronal nicotinic acetylcholine
receptors from cDNA clones identifies a gene family."; Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. "Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholine receptor alpha-subunit."; Nature 319:368-374(1986). 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 41, Last annotation update)
Neutronal acetylcholine receptor protein, alpha-3 chain precursor.
CHRNA3 OR ACRA3.
Rattus norvegicus (Rat). MEDLINE-86118671; PubMed-3753746; Boulter J., Evans K., Goldman D.J., Martin G., Treco D. Helnemann S.F.,

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183 AGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCV
                                                                                                                                                                                                                                                                                                                                                                       495 AA
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InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
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RIFLWVFILVCILGTAGLFL 490
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                                                                                                                                                                                                                                                                        474 RFCLFVFTLFTIIATVAVLL 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PFNUNS; PR00252; NRIONCHANNEL.
TIGRRAMS; TIGR00860; LIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 YQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OF SUBUNITS: ALEHA AND NON-ALPHA (BETA). ALPHA-3 SUBUNIT CAN BE COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 DEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN.
EXTRACELLULAR.
                                                                                        "Characterization of an acetylcholine receptor alpha 3 gene promoter and its activation by the POU domain factor SCIP/Tst-1.";
J. BIOL. Chem. 269:10252-10364(1994).
-1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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N-LINKED (GLCNAC. .) (PROBABLE).
D66C491E832B9C34 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95; Mismatches 177; Indels
                                                   MEDLINE-94193711; PubMed-8144606;
Yang X., McDonough J., Fyodorov D., Morris M., Wang F.,
Deneris E.S.;
Sci. U.S.A. 84:7763-7767(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jé-78;
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Pred. No. le-
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EMBL: U04961; AAA418001.1;
InterPro: IPR006029; Neur_channel_memb.
InterPro: IPR006202; Neur_chan_LBD.
InterPro: IPR006201; Neur_channel_Pfam; PF02931; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
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40.2%;
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                        SEQUENCE OF 1-21 FROM N.A.
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Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
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"Primary structure of an agonist binding subunit of the nicotinic acetylcholine receptor from bovine adrenal chromaffin cells.";
Neurochem. Res. 17:281-287(1992).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONPORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. 01-ocr-1994 (Rel. 30, Created)
1-ocr-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor. -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALLHA AND NON-ALHAM (BETA).
-!- SUBGELLULAR LOCATION: INTEGRAI membrane protein.
-!- SUBGELLULAR LOCATION: THEGRAI MEMBRANE PROTEIN.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 TNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAG 184
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                                                                                                                                                                                                                                                                                                                                                                                            366 ELSNINCFSRIESKVC------KEGYP-----CQDGLCG-YCHHRRAKISNFSANL 409
                                                                                                                                                                                                                                    KNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQ 124
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                                                                                                                                                                                                                                                                                                            185 GDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLI
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Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                  Gaps
                         NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                               BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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P09478; 09VC74;
01-MAR-1989 (Rel. 10, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha-like chain 1 precursor.
NACR-ALPHA-96AA OR ACRE OR ALS OR ACR96AA OR CG5610.
Bursophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta: Pterygota;
                                                                                                                                                              DB 1; Length 495;
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                Indels
                                                                              CYTOPLASMIC (BY SIMILARITY)
                                                                                                                                           322825629821EA07 CRC64;
                                  ALPHA-3 CHAIN.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
POTENTIAL.
                                                                                                                                                                       Pred. No. 4.3e-78;
93; Mismatches 181;
                                                                                                                  (BY SIMILARITY)
                                                                                                                                                              Score 970.5;
                                                                                          POTENTIAL.
                   POTENTIAL.
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470 LWVFILVCILGTAGLFL 486
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                                                                                                                                             56914 MW;
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Best Local Similarity 39.8%
Matches 198; Conservative
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487
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162
495 AA;
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 Receptor;
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RA MEDINE-ZUJABOUGE, BUDMEG-10/31313.

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,

Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

RA Ballaw R.M., Basu A., Barendall J., Bayraktaroglu L., Beasley E.M.,

RA Beson K.Y. Beancs P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Evckstein P., Bolshakov S.,

Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., RA

Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., RA

Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., A

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA

Burtis R.C., Busam D.A., Buller H.W., Glasser K.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dodson K., Doup L.E., Ownes M., Dugan-Rocha S., Dunkov B.C.,

RA Allah M., Kalush F., Gorrell J.H., Gu Z., Kenniston J.A., Ketchum K.A.,

RA Hostin D., Harvey D., Helman T.J., Hernandez J.R., Harris M.,

RA Hostin D., Harvey D., Helman T.J., Wei M.-H., Ideyam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Puri V., Resee M.G.,

RA Relazzollo M., Pittman G.S., Pan S., Pollard J., Puri V., Readen C., Stendton K.A., Nanoshon D.L.,

RA Shue B.C., Siden-Kiamos I. Simpson M., Strong K., Sun E.,

RA Shier E., Spradling A.C., Stapleton M., Strong K., Sun E.,

RA Jazzollo M., Pittman G.S., Langson M., Strong K., Sun E.,

RA Jazzollo M., Pittman G.S., Pan S., Pollard J., Puri V., Rang X., Ranngton W., Wenter J.C., Rangerer E., Spradling A.C., Stapleton M., Strong K., Sun B.,

RA Shier E., Spradling A.C., Stapleton W., Strong K., Shen H.,

RA Sheng X.H., Robong E
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TISSUE SPECIFICITY: CNS IN EMBRYOS.
DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misra S., Crosby M.A., Mungail C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Stapleton M.L., Richter J., Russo S., Schroeder A.J., Shu S.O., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.,
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Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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                                                                                                                            from
                                                                            30ssy B., Ballivet M., Spierer P.; "Conservation of neural nicotinic acetylcholine receptors
                                                                                                                                                              Drosophila to vertebrate central nervous systems. EMBO J. 7:611-618(1988).
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STRAIN=Oregon-R;
MEDLINE-88283626; PubMed=2840281;
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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This SWISS-PROT entry is or between the Swiss Institut the European Bioinformatics use by non-profit institute in entities requires a license or send an email to license or send an email to license selection in the selection of the selection in the s	### And Conservative 9: PHEKRLINALIANYNTLER

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ight. It is produced through a collaboration stiltute. There are no restrictions on its ons as long as its content is in no way not removed. Usage by and for commercial rement (See http://www.isb-sib.ch/announce/b-sib.ch).
                               ||| : | : | : | : | SPGCCPAAAAAAADLSPTFEKP------YAR 475
                                                                                      GPGC----SIFRTDFRRSFVRPSTMEDVGGGLGSHHR 436
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Galliformes, Phasianidae, Phasianinae,
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EVELS IN THE DEVELOPING CILIARY AND
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otation update)
r protein, alpha-3 chain precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77;
a S., Rungger D., Bertrand S.,
and D.;
ha 3. Three clustered avian genes
stylcholine receptor-related
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fefine three distinct neuronal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-MNLKDYWESGEWAIIKAPGYKHDIKYNCCEBIYTDITYSLYIRRLPLFYTINMIIPCL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 LISFLTVLVFYLPSDCGEKVTLCISVLLSLTVFLLVITETIPSTSLVIPLIGEXLLFTM 304
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                                                                                                                                                                                                                                                                                                                                                                                      ALLLTAAVCILFQGCGGSEPEHRLYAALFKNYNQFVRPVKNASDPVIIQFEVSMSQLVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 AGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCV
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                                                                                                ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                           BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                           (bf SIMILARITI).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                                                                     Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 FVTLSIVITVEVLNVHYRTPKTHTMPVWVRTIFLNLLPRIMFMTRP----
                                                        Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                   Mismatches 168;
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EAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFL
                                                                                                                                                                                                                                                                                          Score 948.5; Db 1
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ALPHA-3 CHAIN.
EXTRACELLULAR.
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                                             PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                 CYTOPLASMIC.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGREAMS; TIGR00860; LIC; 1.
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37.78;
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496 AA;
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nes 195; Conserv
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232
264
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214
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P91766;
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Eastham H.W. Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
Eastham H.W. Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
Reynolds S.E., Wolstenholme A.J., Wonnacott S.,
"Characterization of a nicotinic acetylcholine receptor from the insect Manduca sexta.",
Eur. J. Neurosci. 10:879-889(1998).
-:- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPERING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE (BY SIMILARITY). ALPHA-N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL). SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY). 41; Length 516; ACETYLCHOLINE RECEPTOR PROTEIN, Pred. No. 6.1e-76; 84; Mismatches 171; Indel's E7A71E8C45D13BD2 CRC64; EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL) DB 1; SIMILARITY Score 946.5; Pred. No. 6.1 LIKE CHAIN. POTENTIAL. BY SIMILAR POTENTIAL. POTENTIAL POTENTIAL InterPro; IPR006029; Neu_channel_memb. InterPro; IRR006202; Neur_chan_LBD. InterPro; IPR006201; Neur_channel. Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1. PRINTS; PR00252; NRIONCHANNEL. IIGRFAMS; TIGR00860; LIC; 1. Multigene family 58720 MW; 35.9%; 39.7%; EMBL; Y09795; CAA70928.1; -. Conservative 264 2294 326 465 465 223 45 132 233 516 AA; al Similarity 195; Conserv SEQUENCE FROM N.A. 22 244 274 306 327 Transmembrane; TRANSMEM TRANSMEM 193 TRANSMEM TRANSMEM DISULFID DISULFID CARBOHYD CARBOHYD CARBOHYD SEQUENCE Query Match Local SIGNAL DOMAIN DOMAIN CHAIN Matches g g g ò ò δ ò



01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Acetylcholine receptor protein, alpha-like chain precursor (MARAL).

Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm)

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us-09-303-232-6.rsp

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262 312 322 369 427 416 485	Db 417 CDALRRWHRCPELHKAIDGINYIADQTRKEEESTRVKEDWRYVAMVLDRPFLWIFTLAVV 476 Qy 486 IATVAVLLSAP 496 Db 477 vGSAGIILQAP 487	ACH1_SCHGR ID ACH1_SCHGR STANDARD; PRT; 557 AA. AC P23414; AC P23414; DT 01-NOV-1991 (Rel. 20, Created) DT 28-FEB-2003 (Rel. 41, Last annotation update) DE Acetylcholine receptor protein, alpha-L1 chain precursor. DE Acetylcholine receptor protein, alpha-L1 chain precursor. Schistocerca gregaria (Pesert locust). OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; OC Acridoldea; Acridoldea; Orthoptera; Caelifera; Acridomorpha; OX ACRIGORATE ANTD-2010; OX MORT TANTD-2010; DE ACHIOCONTOR ANDD-2010; ON CONTOR TANTD-2010; DE ACHIOCONTOR ANDD-2010; DE ACHIOC	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-91092263; PubMed=1702381; MATShall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W., Darlison M.G., Sattelle D.B., Barnard E.A.; "Sequence and functional expression of a single alpha subunit of an "Sequence and functional expression of a single alpha subunit of an "Sequence and functional expression of a single alpha subunit of an "Sequence and functional expression of a single alpha subunit of an "Sequence and functional repression of a single alpha subunit of an EMBO J. 9:4391-4398(1990).	copyright. It is produced through a collaboration ute of Bioinformatics and the EMBL outstation cs Institute. There are no restrictions on its itutions as long as its content is in no way nt is not removed. Usage by and for commercial see agreement (See http://www.isb-sib.ch/announce/seeisb-sib.ch).	EMBL; X55439; CAA39081.1; - EMBL; X55439; CAA39081.1; - InterPro; IPR006029; Neu_channel_memb. InterPro; IPR0060202; Neur_chan_LBD. InterPro; IPR006202; Neur_chan_LBD. InterPro; IPR006201; Neur_chan_LBD. InterPro; IPR006201; Neur_chan_LBD. InterPro; IPR006201; Neur_chan_LBD. InterPro; IPR00520; Neur_chan_LBD. InterPro; IPR00250; Neur_chan_RBD. InterPro; IPR00250; NEUNCHANNEL. ITGREAMS; TIGR00860; LIC; 1. PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1. Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Iransmembrane; Multigene family. SIGNAL SIGNAL CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1

	7	60	120 124	178 184	232	292 304	350 364	389 424	433	492 526		
CHAIN. EXTRACELLULAR. CYTOPLASMIC. BY SIMILARITY. ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY). N-LINKED (GLCNAC) (POTENTIAL). ALASSER-RICH. ALASSER-RICH. HIS-RICH. MW; 168389C887DFDF3E CRC64;	8; Score 944; DB 1; Length 557;8; Pred. No. 1.1e-75;96; Mismatches 181; Indels 66; Gaps	MAPMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII :	DVDEKNQLLITNIMLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFD :: :	GTYQTNVVVRSGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLV 	LKDEAGGDLSDFITNGEWYLJGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLY : : : : : : : :	YFENLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPL :::	LGTYFNCIMEMVASSVVLTVVVLNYHHFTADIHEMPQMIKSVFLQWLPMILRMSRPGK	-KITRKTIMMNTRMRELELKERSSKSLLANVLDIDDDFRH	RTDFRRSFVRPSTMEDVGGGLGS	-HHRELHLILRELGEITARWKRADEEAELISDWKFAAMVVDRFCLEVFTLFTIIATVAVL :		ARD; PRT; 576 AA. Created) Last sequence update) Cor protein, alpha-like chain 2 precursor. CRE OR SAD OR ACR96AB OR CG6844. Arthropoda; Hexapoda; Insecta; Pterygota; Arthropoda; Brachycera; Muscomorpha;
244 266 2294 329 329 5523 1165 225 225 47 420 63026	35.8% 36.9% ative	LALLPY LLLHH	TNIWE	SGGSCI	AGGDLS VGIDLF	LISSM	MVASSV : TLVGLSV	INTRMRI : : :HAHNSF	STGNLC : SATNRFC	RELQF] HNVLF]		DARD; 5, Cre 5, Las 1, Las tor pr tor pr ACRE ALRE ATHY
24 245 2745 308 330 330 151 151 224 47 47 235 382 56 57 AA;	35. Similarity 36. 1; Conservative	MAPMLAALAI : LPPMLLLLLL	DVDEKNQLLI :: : : DLNLKDQILT	GTYQTNVVVR : VTTMTKAVLH	OKYDDNKVK	YFFNLIVPCV YTVNLIVPCV	LGTYFNCIMF 	-KITRKTIMM : :: ADLASKRLER	GPPPPNST-ASTGNLGPGCSIF 	-HHRELHLII : KYPFELEKAI	LSAP 496 CEAP 530	E STANDARD; 19VC73; 190C73; 190 (Rel. 15, Created) 190 (Rel. 15, Last sequence of the receptor protein. In a melanogaster (Fruit, Metazoa; Arthropoda, Endopterygota; Diptee
DOMAIN TRANSMEM TRANSMEM TRANSMEM DOMAIN TRANSMEM DISULFID DISULFID CARBOHYD CARBOHYD DOMAIN DOMAIN	Query Match Best Local Si Matches 201;	. 5	. 61	121	179 185	233	293	351 365	390	434	493	RESULT 14 ACH2_DROME STANDARD; PRT AC P17644; Q9VC73; DT 01-AUG-1990 (Rel. 15, Last sequen) DT 01-AUG-1990 (Rel. 15, Last sequen) DT 28 FEB-2003 (Rel. 41, Last annota DE Acetylcholine receptor protein, a GN NACR-ALPHA-96AB OR ACRE OR SAD OSOSOPHILA melanogaster (Fruit fl) OC EUKATYOTA; Metazoa; Arthropoda; H OC ROOSTANDARD (Relative Columnia)
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
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Structure and developmental expression of the D alpha 2 g
encoding a novel nicotinic acetylcholine receptor protein
Drosophila melanogaster.";
  Drosophilidae; Drosophila
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-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTERSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-TISSUE SPECIFICITY: CNS IN EMBRYOS.
DEVELOPMENTAL STAGE: LATE EMBRYONIC AND LATE PUPAL STAGES.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY. ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY). N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL). Length 576; 35.7%; Score 943; DB 1; Length 576 36.9%; Pred. No. 1.4e-75; tive 102; Mismatches 189; Indels EXTRACELLULAR (POTENTIAL) N-LINKED (GLCNAC. . .) (P 97D6A46CADC3F42F CRC64; CYTOPLASMIC (POTENTIAL) SUBCELLULAR LOCATION: Integral membrane protein. POTENTIAL. BY SIMILARITY. LIKE CHAIN POTENTIAL. POTENTIAL. PROSITE; PSO0236; NEUROTR_ION_CHANNEL; Receptor; Postsynaptic membrane; Ionic POTENTIAL. Interpro; IPR006029; Neu_channel_memb Interpro; IPR006202; Neur_chan_LBD. Interpro; IPR006201; Neur_channel. PROBABLE FlyBase; FBgn0000039; nAcR-alpha-96Ab Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1 PRINTS; PR00252; NRIONCHANNEL.. Conservative 102; ransmembrane; Multigene family EMBL; X53583; CAA37652.1; -EMBL; AE003748; AAF56303.1; -EMBL; AX058446; AAL13675.1; -PIR; S11679; ACFFA2. 65506 MW; EMBL; X52274; CAA36517.1; -. 65 254 FIGREAMS; TIGRO0860; 576 AA; al Similarity 197; Conserv 262 293 327 MEMBRANE 85 TRANSMEM TRANSMEM Query Match RANSMEM FRANSMEM DISULFID DISULFID CARBOHYD CARBOHYD CARBOHYD SEQUENCE Best Local Matches 19 SIGNAL DOMAIN DOMAIN CHAIN g QQ q

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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                VTTATNRF--SGLVGALGGGLSTLSGYNGLPSVLSGLDDSLSDVAARKKYPFELEKAIHN
          FFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLL
                       TVNLIIPCVGISYLSVLVFYLPADSGEKIALCISILLSQTMFFLLISEIIPSTSLALPLL
                                                                GTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKIT
                                                                                                                     354 RKTIMMNTRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNS-TASTGNLGP-GCS-IF
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TISSUB-Substantia nigra;
MEDLINE-37062879; PubMed-8906617;
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Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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015825;
01-NOV-1997 (Rel. 35, Created)
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Neuronal acetylcholine receptor protein, alpha-6 chain precursor.
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or send an email to license@isb-sib.ch).
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InterPro; IPR006021; Neur_chan_LBD.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006202; Neur_chan_LBD: 1.
Pfam; PF02931; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONGHANNEL.
PROSITE; PS00236; NEUROTE, ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
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GO: 0005892; C:nicotinic acetylcholine-gated receptor-chan. ..;
GO: 00004889; F:nicotinic acetylcholine-activated cation-se. ..;
GO: 00000165; P:signal transduction; TAS.
GO: 00:0006832; P:small molecule transport; TAS.
GO: 00:0006832; P:synaptic transmission; TAS.
                                                                                                                                                    human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: AFTER BINDING ACCTYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN COMPONMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                    IONIC CHANNEL FAMILY.
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BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
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N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Integral membrane protein.
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40.2%; Pred. No. 9e-75;
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EMBL; AB079221; BAC06855.1; -
EMBL; AB079246; BAC06855.1; JOINED.
EMBL; AB079247; BAC06855.1; JOINED.
EMBL; AB079249; BAC06855.1; JOINED.
EMBL; AB079249; BAC06855.1; JOINED.
EMBL; AB079250; BAC06855.1; JOINED.
EMBL; BC014456; AAH14456.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Multigene family
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: ITWTPPAI 153	NGEWYLIG 200	NSEWEIID 210	TLPPDSGE 260	YLPSDCGE 270	VVLNYHHR 320	FVLNIHYR 330	SKSLLANV 380	AKGKLAS- 385	TMEDVG 428	QWVVEN 422	TLFTIIAT 488	INCVEGT 479		
	FKSTCKMDIAMFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNCEWYLIG	FKSSCPMDITFFPFDHQNCSLKFGSWTYDKAEIDLLIIGSKVDMNDFW	MPGKKNIITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGE	ASGYKHDIKYNCCE	KLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFWVASSVVLTVVVLNYHHR	KVTLCISVLLSTTVFLLVITETIPSTSLVVPLVGEYLLFTMIFVTLSIVVT		TPTTHTMPRWVKTVFLKLLPQVLLMRWPLDK-TRGTGSDAVPRGLARRPAKGKLAS-	LDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVRPSTMEDVG 428	HGEPRHLKECFHCHKSNELA	429 GGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCLFVFTLFTIIAT	423SEHSPEVEDVINSVQFIAENMKSHNETKEVEDDWKYVAMVVDRVFLWVFIIVCVFGT	489 VAVLL 493	AGLFL 484
94	143	154	201	211	261	271	321	331	381	386	429	423	489	480
qa	٥y	g	Qy	qq	Qy	qq	Qy	qa	Qy	qq	δy	qa	οy	qq

Search completed: August 13, 2003, 15:26:13 Job time: 12.4907 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 15:21:45; Search time 18.7131 Seconds (without alignments) 2574.698 Million cell updates/sec Run on:

US-09-303-232-6 2640 1 MAPMLAALALLALLPVSEQG......LFTIIATVAVLLSAPHIIVQ 501 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	1260	47.7	7 502	-	ACHUA7	nicotinic acetylch
7	1255.5	47.6	5 502	~	A57175	nicotinic acetylch
ĸ	1253	47.5		~	JN0113	nicotinic acetylch
4	1252.5	47.4		7	G02259	alpha 7 neuronal n
S	1246.5	47.2		7	T01378	nicotinic receptor
9	1237.5	46.5		~	. S68588	nicotinic acetylch
7	1226.5	46.5	5 511	7	JH0173	alpha-bungarotoxin
80	1132	42.5		~	T25671	hypothetical prote
6	1083.5	41.0		~	T19862	hypothetical prote
10	1081	4		~	T19622	
11	686			7	A53956	Ψ
12	982.5	37	•	~	A37040	nicotinic acetylch
13	970.5			~	860589	acetylcholine rece
14	970.5			N	A24572	nicotinic acetylch
15	964.5			-	ACFFA1	nicotinic acetylch
16	944	35.8		~	S12359	nicotinic acetylch
17	943	35.7		-	ACFFA2	nicotinic acetylch
18	929.5	35.		~	T09289	
19	924.5	35.(Н	ACCH2N	nicotinic acetylch
20	919.5	34.8		N	B37014	
21	919	34.8		~	A40110	
22	910	34.5		~	S12899 ·	nicotinic acetylch
23	909.5	34.5		~	B35721 ·	nicotinic acetylch
24	906.5	34.3		7	A30992	probable nicotinic
25	906	34.3		-	ACBOA1	nicotinic acetylch
26	905	34.3			ACHUA1	nicotinic acetylch
27	901	34.1		Н	ACFFNN	nicotinic acetylch
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29	897.5	34.0) 627	7	JC4021	nicotinic acetylch

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456	205	622	457	470	625	498	459	457	445	491	461	461	457	457	559
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968	895	891	890	890	888	887	885.5	882	883.5	881	879.5	876.5	875.5	869.5	862
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal F;24-502/Product: transmembrane #status predicted <TR1>F;262-280/Domain: transmembrane #status predicted <TR2>F;262-280/Domain: transmembrane #status predicted <TR3>F;26-317/Domain: transmembrane #status predicted <TR3>F;470-488/Domain: transmembrane #status predicted <TR4>F;46.90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted F;150-164/Disulfide bonds: #status predicted (F;150-164/Disulfide bonds: #status predicted (F;155/413/Binding site: phosphate (Ser) (covalent) #status predicted F;415/Binding site: phosphate (Thr) (covalent) #status predicted

; 9 Gaps 50; Query Match 47.7%; Score 1260; DB 1; Length 502; Best Local Similarity 48.5%; Pred. No. 2.6e-99; Matches 247; Conservative 75; Mismatches 137; Indels 5

. Qy 12 ALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKNQLLIT :	NQLLIT 71 : NQVLTT 74	Qy Db	67 QLLITNIMLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126 : :
Oy 72 NIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTNVVVTRS	NVVVRS 131 : NVLVNS 134	Oy DD	127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNOLDLVLKDEAGGD 186
QY 132 GGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDLSDFI 	DLSDFI 191 	Qy	187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246
QY 192 TNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISSMALLG	SMALLG 251 :: · ALALLV 251	Oy Db	247 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMEMVAS 306
QY 252 FTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLT	SSWLT 311 : LSWVT 311	Oy Db	307 SUVLTUVVLNYHRTADIHEMPOMIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366
OY 312 VVVLNYHHRTADIHEMPOWIKSVFLQWLPWILRWSRPGKKITRKTIMMNTRNRELELKER	LELKER 371 	dg .	367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRKS 417
Qy 372 SSKSLLANVLDIDDDFRHGPPPRNSTASTGNL	-GPGCSIFRT 412 	oy da	418 FVRPSTMEDVGGGLGSHHRELHLILRELØFITARMKKADEBABLISDWKFAAMVVDRFCL 477 1 : :
QY 413 DFRRSFVRPSTMEDVGGGLGSHHRELHLILRELQFITARWKRADEEAELJSDWKFAAM	DWKFAAM 470 :11111 EWKFAAC 465	Qy Db	478 FVFTLFTIATVAVLLSAPHII 499 :: : : : : : 473 MAFSVFTIICTIGILMSAPNFV 494
OY 471 VVDRFCLFVFTLFTIIATVAVLLSAPHII 499 		RESULT 3 JN0113 nicotinic	: acetylcholine receptor alpha-7 chain precursor, neuronal - chicken te names: alpha-bungarotoxin-binding protein alpha chain
RESULT 2 A57175 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999 C;Accession: A57175 R;Orr-Uttreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.		C; Species: C; Date: C; Caccess R; Coutur R; Coutur A; Title: A; Referen	C; Species: Gallus gallus (chicken) C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999 C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999 C; Accession: JN0113; JH0172; S28018; B25738; S2656 R; Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N Neuron 5, 847-856, 1990 A; Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is development A; Reference number: JN0113; MUID:91097796; PMID:1702646
Clouds and mapping of the mouse alpha7-neuronal nicotinic clouds and mapping of the mouse alpha7-neuronal nicotinic oce number: A57175; MUID:95324936; PMID:7601470 in A57175 in Preliminary preliminary e type: mRNA	acetylcholine recept	A; Molecus A; Residuc A; Cross-1 A; Experin R; Schoep	Le type: DNA as: 1-502 <coud. references: GB:X68586; NID:9287756; PIDN:CAA48576.1; PID:9287757 nental source: White Leghorn; brain fer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.</coud.
A; residues: 1-502 < COKK> A; Cross-references: 08:L37663; NID:9790853; PIDN:AAC42053.1; PID:9790854 C; Superfamily: acetylcholine receptor C; Keywords: brain; 91ycoprotein; ion channel; neurotransmitter receptor;	54 r; phosphoprotein;	A;Title: A;Refered A;Access	, 33-48, 1390 Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtypes of t nce number: JH0172, MUID:90315158; PMID:2369519 ion: JH0172.
F:123/Domain: signal sequence #status predicted <sig> F:14-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal F:231-254/Domain: transmembrane #status predicted <tr1> F:262-280/Domain: transmembrane #status predicted <tr2> F;296-317/Domain: transmembrane #status predicted <tr3></tr3></tr2></tr1></sig>	#status predi	A; Molecu. A; Residue A; Cross-1 A; Experir R; Matter	le type: mRNA ss: 1-502 <scha. references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078 mental source: brain Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M.</scha.
F:470-48B/Domain: transmembrane #status predicted <tra> F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted F:415/Binding site: phosphate (Thr) (covalent) #status predicted F:442/Binding site: phosphate (Thr) (covalent) #status predicted</tra>		EMBO J. A,Title: A,Referel A,Access A,Molecu	EMBO J. 11, 4229-4538, 1992 Ayitile: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter A.Reference number: S28018; MUID:93049204; PMID:1425587 A.Rocession: S28018 A.Molecule type: DNA
Query Match 47.6%; Score 1255.5; DB 2; Length 502; Best Local Similarity 49.6%; Pred. No. 6.3e-99; Matches 249; Conservative 78; Mismatches 148; Indels 27; Gaps Qy 8 LAL-LALLPVSEQGPHEKRLINALLANYTLERPVANESEPLEVREGLTLQQIIDVDEKN :: ::	Gaps 7; DVDEKN 66 DVDEKN 69	A, Residues: A, Cross-reff A, Experiment B, Conti-Troi Proc. Natl. A, Title: Brance A, Reference A, Recession A, Molecule	A; Residuees: 1-18 < MAS> A; Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320 A; Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320 A; Experimental source: White leghorn; erythrocyte R; Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985 A; Title: Brain and muscle nicotinic acetylcholine receptors are different but homolog A; Reference number: A94055; MUID:85270494; PMID:3860855 A; Accession: B25738 A; Molecule type: protein

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47.4%;
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                                                                    C. Superfamily: acetylcholine receptor (C. Keywords: brain: 930/3)
C. Superfamily: acetylcholine receptor (C. Keywords: brain: glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein; F: 1-23/Domain: signal sequence #status predicted <SIG> F: 24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted <F: 254-802/Domain: transmembrane #status predicted <TR1> F: 252-80/Domain: transmembrane #status predicted <TR2> F: 262-80/Domain: transmembrane #status predicted <TR3> F: 46.90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted F: 355,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted F: 415/Binding site: phosphate (Thr) (covalent) #status predicted F: 442/Binding site: phosphate (Thr) (covalent) #status predicted
                         and is localized
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFRRSFVRPSTMEDVGGGLGSHH-----RELHLILRELQFITARMKKADEEAELISDWKF 467
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C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha 7 neuronal nicotinic acetylcholine receptor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999 C;Accession: G02259 R;Leonard, S. submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: |||:| | | | |:|||||||:| :::
TFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQKCNLKFGSWTYGGWSLDLQMQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| |||:||:|| || | | :||:||: | | ||||: | |||: | | |||: | |||: || IIVGLSVVVTVIVIQYHHDPDGGKMPKWTRVILLINWCAWFLRMKRPGEDKVRPACQHKQ
                                                                                                                                                                                                                                                                                                                                                                                                 APMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQ11D
                                                                                                                                                                                                                                                                                                                                                                                                                      VDEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKD
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                                                                                                                                                                                                                                                                                                                                                               Gaps
Residues: 24-25, ET', 28-41, 'X', 43-45, 'X', 47 <CON>; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin
                                                          80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                         Length 502;
                                                                                                                                                                                                                                                                                                                       47.5%; Score 1253; DB 2; Length 5(
48.8%; Pred. No. 1e-98;
tive 81; Mismatches 145; Indels
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A;Molecule type: mRNA
A;Residues: 1-502 <LEO>
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                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 48.8
Matches 250; Conservative
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A; Accession: G02259
                                                        A; Introns: 19/1; 65/3;
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distribution of rat brain alph 7 7; 246 246 366 407 407 G------RMACSPTHDEHLLHGCQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460 QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306 306 366 465 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186 126 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186 69 99 69 C, Accession: T01378
R; Sequela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A; Title: Molecular cloning, functional properties, and distribution of rat b A; Reference number: 214310; MUID: 93147931; PMID: 7678857
A, Accession: T01378
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-502 <SEG>A; Cross-references: EMBL: S53987; NID: 9264770; PIDN: AAB25224.2; PID: 95705903
A; Experimental source: brain
C; Superfamily: acetylcholine receptor nicotinic receptor alpha 7 chain - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 367 ASVEMSAVA------PPPSGVVC LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN SIFRIDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW 8 LAL-LALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 51; Indels 27; Length 502; Length Indels 5; DB 2; 140; 149; 5; DB; 1.1e-98; 466 KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499 Query Match 47.2%; Score 1246.5; DB Best Local Similarity 49.4%; Pred. No. 3.7e-98; Matches 248; Conservative 78; Mismatches 149 ELKERSSKSLLANVLDIDDDFRHGPPPPRSTASTGNL 74; Mismatches Score 1252.5; Pred. No. 1.16

a	: : : : : : :	qa	: : : : :::
Qy Db	187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246 : : :	Qy	359 MNTRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCS 408 : :
Qy Db	247 MALLGETLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306 	do Db	409 IFRTDFRRSFVRPSTMEDVGGLGSHHRELHLILRELQFITARMKRADEEAELIS 463
Oy Db	307 SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366 	Oy Dp	464 DRKFAAMVVDRECLEVETLETITATVAVLLSAPHII 499 :
Qy Db	367 ELKERSSKSLLANVLDIDDDFRHGPPPRSTASTGNLGPGCSIFRTDFRRS 417 1	RESULT JH0173	of contract of the contract of
. Хо да	418 FVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKRADEEAELISDWKFAAMVVDRFCL 477	alpha-bun C;Species C;Date: 3 C;Accessi	Dinding process aspirate chais precessor allus (chicken) **sequence_revision 31-Dec-1991 *text_chan
Qy	478 FVFTLFTIIATVAVLLSAPHII 499 	R; Schoe Neuron A; Title A; Refer	R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J. Neuron 5, 35-48, 1990 A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtypes of t A;Reference number: JH0172; WUID:90315158; PMID:2369519
S C	9	A; Acces A; Molec A; Resid	
S68588 nicotir C;Speci	nic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis elegans Hes: Caenorhabditis elegans - 06-nec-1906 #sequence revision 07-pep-1997 #fext change 20-Aug-1999	A;Cross A;Exper: A;Note: C:Comme	references: GB:X22296; NID:g03001; FIDN:CAA30344.1; FID:90300 imental source: brain this sequence is similar to acetylcholine receptor alpha chai t: Alpha-bungarotoxin binding proteins are localized to extra
C; Acces R; Ball: J. Mol.	ertrand, D.	C; Super C; Keywo F; 1-30,	od <sig></sig>
A;Titl(A;Refel A;Acces A;Statu	A;Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans. A;Reference number: \$68587; MUID:96196478; PMID:8627624 A;Accession: \$68588 A;Status: nucleic acid sequence not shown A:Molecule tyne: mRNA	F; 31 - 51 F; 239 - 2 F; 270 - 2 F; 304 - 3 F; 479 - 4	בסרמה להומחורה
A; Resid	Festiques: 1-498 GABLD Cross-references: EMBL:X83887; NID:9872087; PIDN:CAA58764.1; PID:9872088	F; 54/B.	site: carbohydrate (Asn) (covalent) #status
C; Super C; Keywc F; 1-19/	Д	Query M Best Lo Matches	atch cal Similarity 46.6%; Pred. No. 1.9e-96; 246; Conservative 75; Mismatches 134; Indels
F;20-498/F Query Ma Best Loc	D D	Qy	5 LAALALLALLPVSEQGPHEKRLINALLANYNTLERPVANESEPLEVRFGLTLQOIIDVDE 64
Matc) Qy	245; Conservative 2 APMLAALALLALLPV	Qy du	65 KNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADBGFDGTYQ 124 : : : : : : :
oy Oy	15 APTIGSLQERRIYEDLARNYNNIERPYNHSEPYTYHLKYALQQIID 61 62 VDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWRPDVLMYNSADEGFDG 121	ον το το	
qq	62 VDEKNQVYVNAMLDYTWNDYNLVWDKAEYGNITDVRFPAGKIWRPDVLLYNSVDTNFDS 121	gg ko	GDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLI
ر ان ان ا	122 TYQTNVVRSGGSCLXVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKD 181 123 THIII::	ු අ	
ν̈́δο	EAGG-DLSDEITHGEWYLIGMDGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP	ος Q	245 SSMALLGETLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFWV 304 : : : :
a 6	180 ATGGFDISEYISNGEWALFLTTVERNEKFYDCCFEPYPDVHFYLHWRRTLYYGFNLIMP 239 241 CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300	QY	ASSVVLTVVVLNYHHRTADIHEMPOMIKSVFLOWLPWILRMSRPGKKITRKTIMMNTRMR
g qa	:	<u>අ</u>	313 GLSVVVTVLVLQFHHHDDQAGKMPRWVRVILLNWCAWFLRMKKPGENIK 361 365 ELELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNLGPGCSIF 410
Οy	301 MFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIM 358	3	::

us-09-303-232-6.rpr

qq	362 PLSCKYSYPKHHPSLKNTEMNVLPGHQPSNGNMIYSYHTMENPCC 406	
Qy Db	411 RTDFRRSFVRPSTMEDVGGGLGSHHRELHLILRELQFITAR 451	RESULT 9 T1986. hypothetical protein C40C9.2 - Caenor C;Species: Caenorhabditis elegans
Oy do	452 MKKADEEAELISDWKFAAWVDRFCLFVFTLFTIIATVAVLLSAPHII 499 	C:Date: 15-Oct-1999 #sequence_revisio C:Accession: T19862 R:Hembry, C. R:Hembry, C. S:Dmitted to the EMBL Data Library, M
RESUL!		A; Relevence number: 4,5155 A; Accession: T19862 A; Status: preliminary; translated fro
hypotl C; Spec C; Date	netical protein D2092.3 - Caenorhabditis elegans ies: Caenorhabditis elegans :: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000	A:Wolecule type: DNA A:Residues: 1-542 <wil> A:CROSS references: EMBL:270265; PIDN A:Experimental source: clone C40C9</wil>
C; Acco R; Gat1 submit A; Desc A; Refé	C; Accession: T25671 R; Gattung, S.; Maggi, L. submitted to the EMBL Data Library, February 1997 A; Description: The sequence of C. elegans cosmid D2092. A; Reference number: 220067	C;Genetics: A;Gene: CESP:C40C9.2 A;Map position: X A;Introns: 11/3; 69/3; 123/2; 173/3; C:Suberfamily: acetvicholine receptor
A; Acc. A; Staf A; Mole A; Res		Query Match Query Match Best Local Similarity 42.6%; Pre Matches 232; Conservative 86;
A; Exp. C; Gene A; Gene	is-reterences: Embi.00010/; FlDN.AAB4223.1; GSPDB:GNUUU19; CESP:DZU92.3 timental source: strain Bristol N2; clone D2092 tics: CESP:D2092.3	Qy 10 LLALLPVSEQGPHEKRLLNALLA
A;Map A;Inti C;Supe	position: 1 ons: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2 rfamily: acetylcholine receptor	
Que Best Matc	Query Match 42.9%; Score 1132; DB 2; Length 461; Best Local Similarity 44.7%; Pred. No. 1.9e-88; Matches 216; Conservative 86; Mismatches 127; Indels 54; Gaps 6;	
Qy	23 EKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKNQLLITNIWLSLEWNDY 82 :	137
γo.	14	Db 197 SDEGIDVQYYVQNGEWNLLAVPA Qy 241 CVLISSNALLGFTLPPDSGEKLT
3 % 1		Db 255 SFLISLMTVLGFTLPPDAGEKIT Qy 295 TYFNCIMPMVASSVVLTVVVLNY
o vo	14% GVLKEVCÇLDVTWEPEDDQVCEMKEGSWTEHGYAIDLQIDDDTNGTQSMDLSTYLVNGEW 205 197 YLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISSMALLGFTLPP 256	315
qq :		QY 355 KIIMMNIKMKELELKEKSKSLL :: : :: : : : : : : : : :
d d	25) DSGEKLITAVILLALIVYELNIASTLEPONSDAIPELGIYENCIMEMANSSWVILTAVVUN 316 26 DAGEKITLEVILLIAIVFFLSANVEBMTPPTSBAVPLIGVFFSCCMLVVSASVVFTIVVLN 325	413
Ολ	YHHRTADIHE	Db 417 IKLGRQQTIDFEYEFHVQHNHLM Ov 439 HLILRELOFITARMKKADEEAE-
q :	LHFRSADSHEMNPLVRRVLLEFLPWLLFMSRPGYKFVK	477
À q	3// LANYLDIDDERRIGPPPRSTASTGNLGPGCSIFRTDFRRSFVRPSTMEDVGGGLGSHHR 436	495 APHII
Oy Op	437 ELHLILRELQFITARMKKADEEAELISDWKFAAWVDRFCLFVFTLFTIIATVAVLLSAP 496 : : : : :	DD 537 SPHLI 541 RESULT 10
oy Db	497 HII 499 1	T19622 hypothetical protein C31H5.3 - Caenor C; Species: Caenor C: Species: Caenorhabditis elegans
1	110	C;Date: ID-OCC-IMMA #Sequence_revision

216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; LILGVIILLSLIVFLNLVAETLPQVSDAIPLL----G 294 GKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP 240 SECTION STREET S IDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDL 187 IYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITR 354 LANVLDIDDDFRHGPPPNSTASTGNLGP--GCSIFRT 412 MPVAPSEMTPRVTYSKVMAESYVEDVVMTELNKYMQKA 476 DN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2 on 15-Oct-1999 #text_change 18-Feb-2000 on 15-Oct-1999 #text_change 21-Jan-2000 ced. No. 3.2e-84; Mismatches 152; Indels 75; orhabditis elegans rhabditis elegans OM GB/EMBL/DDBJ March 1996 C; Accession: T19622

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A; Cross-references: EMBL: X53559; NID: g34985; PIDN: CAA37625.1; PID: g34986
                                                                                                                                                                                                GDB:125219; OMIM:118503
                                                                                                                                                                                                 A;Cross-references: GDB:125219; OMIN:3
A;Map position: 15q2+15q2
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor
                                                                                                     A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 30-503 <ANA>
A; Residues: 1-503 <MIH>
                                                                                                                                                                   C; Genetics:
A; Gene: GDB: CHRNA3
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C;Species: Homo sapiens (man)
C;Date: 07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change 20-Aug-1999
C;Accession: A59956; S21338
R;Mihovilovic, M.; Roses, A.D.
R;Mihovilovic, M.; Roses, A.D.
A;Title: Expression of mRRMs in human thymus coding for the alpha3 subunit of a neuronal A;Reference number: A53956; MUID:91114756; PMID:1989896
A;Accession: A539556
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILTRPNGNGHSAVDKAVHLDLSTGNPHSDAKKSSPSPKRTSASIMGMTG------ 433
                                                                                                                                                                                                                                                                                                                                                     80 NDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTNVVVRSGGSCLYVP 139
                                                                                                                                                                                                                                                                                                                                                                       PGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNGEWYLI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                   GMPGKKNTITYACCPEPYVDVTFTIMIRRRLLYYFFNLIVPCVLISSMALLGFTLPPDSG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTADIHE-MPQWIKSVFLQWLPWILRMSRP------GKKITRKTIMMNTRMR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: : :: | :::|:: | |||| :| | ||
RSPEQYKPMNKFLKTLLLGWLPTLLGMERPDVLELSVHGAHYASDNKKQRQYLIEVERH 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELELKERSSKSLLANVLDID-----DDFRHGPPPPNSTAST--GNLGPGCSIFRTDFR 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LPTT---QMNGALDSSINKYTCTKVTRPLENGSATINHKSSPQINPINNNIYKCAN 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-560 <WIL>
A;Coss-references: EMBL: 293778; PIDN:CAB07843.1; GSPDB:GN00019; CESP:C31H5.3
A;Experimental source: clone C31H5
                                                                                                                                                                                                                                                                                          20 GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKNQLLITNIWLSLEW 79
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                Length 560;
                                                                                                                                                   A;Gene: CESP:C31H5.3
A;Map position: 1
A;Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                            Score 1081; DB 2;
Pred. No. 5.5e-84;
3; Mismatches 155;
               Library, April 1997
                                                                                                                                                                                                                                                            88;
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         Similarity
 R;Kershaw, J.
submitted to the EMBL
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Best Local
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C; Genetics:
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Matches
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                                                                                                                                                                                                                                                                                                                                                             61 DVDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFD 120
                                                                                                                                                                                                                                                                                                                                121 GTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 TRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL····-GPGCS···· 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----IFRTDFRRSFVRPSTMEDVGG--GLGSHHRELHLILRELQFITARMKK 454
                                                                                                              1 MAPMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII 60
                                                                                                                                                                 20
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C;Accession: A37040; S24592
R;Fornasari, D; Chini, B.; Tarroni, P.; Clementi, F.
Neurosci. Lett. 111, 351-356, 1990
A;Fitle: Molecular cloning of human neuronal nicotinic receptor alpha-3-subu A;Reference number: A37040; MuID:90245296; PMID:2336208
A;Reference number: A37040
A;Reference receptor alpha-3-subu A;Reference number: A37040; MuID:90245296; PMID:2336208
A;Reference number: BA7040
A;Residues: 1-502 <FORD
A;Residues: 1-502 <FORD
A;Residues: 1-502 <FORD
                                                                                                                                             181 DEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TSNEGNAQKPRPLYGAELSNLNCFSRAESKGCKEGYPC
                                                           Gaps
                                                        62;
     Length 503;
37.5%; Score 989; DB 2; Length 50
38.9%; Pred. No. 3.3e-76;
Live 91; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 ADEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLL 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.5%
Best Local Similarity 38.9%
Matches 202; Conservative
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us-09-303-232-6.rpr

C;Superfamily: acetylcholine receptor C;Keywords: neurotransmitter receptor; transmembrane protein F;1-28/Domain: signal sequence #status predicted <sig> F;29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted <mat></mat></sig>	OY 65 KNQLLITNIMLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQ :: : : : : : : : : : : :	TPNKLMKPDVLMYNSADEGFDGTYQ 124 : :: : PAEKIWKPDIVLYNNAVGDFQVDDK 126
Ouery Match 37.2%; Score 982.5; DB 2; Length 502; Best Local Similarity 38.9%; Pred. No. 1.2e-75; Matches 199; Conservative 89; Mismatches 163; Indels 61; Gaps 5;	OY 125 TNVVVRSGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAG ::: ::	HCDMKFGSWTYDGNQLDLVLKDEAG 184
QY 8 LALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKNQ 67 1 1 1 1 1 1 1 1 1	QY 185 GDLSDFITNGEWYLIGMPGKKNTITYACCPEDYVDVTFTIMIRRRTLYYFFNLIVPCVLI :	YVDVTFTIMIRRRTLXYFFNLIVPCVLI 244
QY 68 LLITNIMLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKRDDVLMYNSADEGFDGTYQTNV 127 ::	QY 245 SSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFWV : :	AETLPQVSDAIPLLGTYFNCIMFMV 304
OY 128 VVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGDL 187 ::: ::	QY 305 ASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNT :	**************************************
Qy 188 SDFITNGEWYLLGMPGKKNTITYACCPEPYVDVFFIMIRRRTLYYFFNLIVPCVLISSM 247 : : : :	QY 362 RMRELELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNLGPGGSIFRTDFRRSF	TASTGNLGPGCSIFRTDFRRSF 418
OY 248 ALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTVFNCIMEMVASS 307 :	OY 419 VRPSTMEDVGGGLGSHHRELHLILRELQFITARWKKADEEAELISDWKFAAMVVDRFC	MKKADEEAELISDWKFAAMVVDRFC 476
OY 308 VVLTVVVLNYHHRTADIHEMPOMIKSVFLOMLPWILRNSRPGKKITRKTIMMNTRMRELE 367 : :	Oy 477 LEVETLETIATVAVLL 493	
QY 368 LKERSSKSLLANVLDIDDDFRHGPPPRNSTASTGNLGPGCS	RESULT 14 A24572	
409IFRIDERRSFVRPSTMEDVGGGLGSHHRELHLILRELQFITARMKADEBAEL 461 1	nicolinic acetylcholine receptor alpha-3 chain precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 08-Nov-1996 C;Accession: A24572	ecursor - rat 8 #text_change 08-Nov-1996
Qy 462 ISDWKFAAMVVDRFCLEVFTLFTIIATVAVLL 493 	R.Boulter, J.; Evans, K.; Goldman, D.; Martin, G.; Treco, D.; Heinemann, Mautre 319, 368-374, 1986 Mature 319, 368-374, 1986 A.Title: Isolation of a cDNA clone coding for a possible neural nicotinic A.Reference number: A24572; MUID:86118671; PMID:3753746 A.Accession: A24572	; Treco, D.; Helnemann, S.; Patrick, ossible neural nicotinic acetylcholl 753746
RESULT 13 \$60589 acetylcholine receptor alpha chain precursor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999	A; Molecule type: mRNA A; Residues: 1.499 < < > < < > < < > < < > < < > < < > < < > < < > < < < > < < < > < < < > < < < < > < < < < < < < > < < < < < < < < < < < < < < < < < < < <	mitter receptor; postsynaptic membra <sig> r alpha chain #status predicted <mat< td=""></mat<></sig>
R;Criado, M.; Alamo, L.; Navarro, A. Neurochem. Res. 17, 281-287, 1992 A;Title: Primary Structure of an agonist binding subunit of the nicotinic acetylcholine A;Reference number: 560589: MITD:02319195: DWID:152021	Query Match 36.8%; Score 970.5; DB 2 Best Local Similarity 39.6%; Pred. No. 1.2e-74; Matches 199; Conservative 91; Mismatches 180	DB 2; Length 499; 2-74; 180; Indels 33; Gaps 7;
A; Accession: \$60589 A; Status: preliminary A; Molecule type: mRNA A posiding: 1.405 CPT	OY 3 PMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDV 1: : 1 1 1 1 1 1 1 1 1	LERPVANESEPLEVREGLTLQOIIDV 62 : : :: :: :: IIRPVANVSHPVIIQFEVSMSQLVKV 68
A; Cross-references: EMBL.X57032; NID:g297762; PIDN:CAA40348.1; PID:g297763 C; Superfamily: acetylcholine receptor C; Keywords: neurotransmitter receptor F:1-21/Domain: signal sequence #status predicted <sts></sts>	QY 63 DEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGT	ILRITPNKLWKPDVLMYNSADEGFDGT 122 : : :
oduct: acetylcholine receptor alpha of	QY 123 YQTNVVVRSGGSCLYVPPGIFKSTCKMDIAMPPEDDQHCDMKFGSWTYDGNQLDLVLKDE ::	DQHCDMKFGSWTYDGNQLDLVLKDE 182 : : :: YQNCTMKFGSWSYDKAKIDLVLIG- 187
Matches 198; Conservative 93; Mismatches 181; Indels 25; Gaps	183	
Qy 5 LAALALLAVSEQGPHEKRLINALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDE 64	Db 188 SSMNLKDYWESGEWAIIKAPGYKHEIKYNCCEEIYQDITYSLYIRRLPLFYTINLIIPCL Oy 243 LISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMF	ODITYSLYIRRLPLEYTINLIIPCL 247 LVAETLPQVSDAIPLLGTYFNCIMF 302

QY 193 NGEWYLIGMPCKKNTITYACCPEPYUDYFFILMIRRFLYYFFNLIVPCVLISSMALLGF 252 1 1 1 1 1 1 1 1 1	OY 395 NSTASTGNLGPGCSIFRTDFRRSFVRPSTWEDVGGGLGSHHR 436	476 497 536	Search completed: August 13, 2003, 15:30:22 Job time : 19.7131 secs						
248 LISFLTVLVFYLPSDCGEKVTLCI 303 MVASSVVLTVVVLNYHHRTADIHE 1 1:1 1 1 1 1 308 FVTLSIVITVFVLNVHYRTPTTHT 360 NTRMRELELKERSSKSLLANVLDI 368 GAELSNLNCFSRCRLQKLQGRL- 413 DFRRSFVRPSTMEDVGGGLGSH 6	Qy 471 VVDRFCLEVFTLFTIATVAVLL 493 L:	ACFFA1 nicotinic acetylcholine receptor alpha-1 chain precursor - fruit fly (Drosophila melanog C; Species: Drosophila melanogaster C; Species: Droc-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002 C; Accession: S00381; A38801 R; Bossy, B., Ballivet, M.; Spierer, P. EMBO J. 7, 611-618, 1988	A;Title: Conservation of neural nicotinic acetylcholine receptors from Drosophila to ver A;Reference number: \$00381; MUID:88283626; PMID:2840281 A;Accession: \$00381 A;Molecule type: DNA A;Residues: 1.567 ABOS>	A;Coss-retelences: OB:AU/194; N.D:g/3/3; Fibn:CAR301/2.1; Fib.g/3/3; A;Accession: A38801 A;Accession: A38801 A;Molecule type: mRNA A;Reaidues: 1-567 - 6202> A;Cross-references: EMBL:XO7194; NID:g7575; PIDN:CAA30172.1; PID:g7576 A;Note: 538-Tyr was also found C;Genetics: A;Gene: Flysase:nAcR-alpha-96Aa	A;Cross-references: Flybase:FBgn0000036 A;map position: 3R 96A A;introns: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3 C;Superfamily: acetylcholine receptor C;Keywords: glycoprofein; ion channel; neurotransmitter receptor; postsynaptic membrane; F;1-21/Domain: signal sequence #status predicted <sigs #status="" <ext="" <f;22-240="" acetylcholine="" alpha-like="" chain="" domain:="" extracellular="" f;2-567="" nicotinic="" predicted="" product:="" receptor=""> F;22-240/Domain: transmembrane #status predicted <tm1> F;27-290/Domain: transmembrane #status predicted <tm1></tm1></tm1></sigs>	F;306-325/Domain: transmembrane #status predicted <tm3> F;326-513/Domain: intracellular #status predicted <int> F;326-513/Domain: transmembrane #status predicted <int> F;514-532/Domain: transmembrane #status predicted <tm4> F;45,233/Binding site: carbohydrate (Asn) (covalent) #status predicted F;149-163,222-223/Disulfide bonds: #status predicted</tm4></int></int></tm3>	Query Match Query Match Best Local Similarity 36.5%; Pred. No. 4.8e-74; Best Local Similarity 36.5%; Pred. No. 4.8e-74; Matches 198; Conservative 95; Mismatches 158; Indels 91; Gaps 9; Qy 21 PHEKRLINALLANYNTLERPYANESEPLEVREGITLQOIIDVDEKNOLLITNIMLSLEWN 80 Db 23 PDAKRLYDDLLSNYNKLRPYGNNSDRLYVKAGLRLSQLIDVNIKNOLMYTNVWYSOEWN 82	81 DYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYGTNV	QY 14.1 GIRKSTCKMILAMEFUNDHUMENGSWITDONGLDE VEND 1.1.1 1.1.1 1.1.1 1.1 1.1 1.1 1.1 1.1

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August 13, 2003, 15:14:30 ; Search time 43.9474 Seconds (without alignments) 1809.483 Million cell updates/sec
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                              OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Description	H virescens agety	H. virescens acety	D. melanogaster ac	Drosophila melanog	Drosophila melanog	Human neuronal nic	Neuronal nicotinic	Human PRO2145 prot	Nicotinic acetylch
SUMMARIES	AAY50816	AAY50815	AAY50814	ABB60432	ABB63683	AAW44153	AAW09025	AAB24088	AAB82690
	21	21	21	22	22	15	18	21	22
% Query Match Length DB	501	496	770	498	311	502	502	502	502
% Query Match	100.0	68.3	6.09	59.5	48.6	47.7	47.7	47.7	47.7
Score	2640	1803.5	1609	1570.5	1283	1258.5	1258.5	1258.5	1258.5
Result No.	1	2	m	4	ស	9	7	80	σ

Wild-type human al	neuronal NAC	neuronal nic	V274T variant huma	alpha-bun	human alpha	human alpha	human alpha	alph	Caenorhabditis ele	bditis ele	nicotinic	Chimeric alpha7/5-	uronal NAC	uronal nic	Drosophila melanog	ell surfac	Human neuronal nic	Neuronal nicotinic	uronal NAC	neuronal nic	Drosophila melanog	neuronal nic	2 subunit of	Neuronal nicotinic	neuronal NAC	neuronal nic	Prostate cancer-as	bditis ele	bditis ele		acetylcho	hen ACR s	nicotinic		la melanog
Wild-typ	Human ne	Human ne	V274T va	Neuronal	Mutant h	Mutant h	Mutant h	Neuronal	Caenorha	Caenorhabditis	Neuronal	Chimeric	Human neurona	Human neuronal	Drosophi	Mature cell	Human ne	Neuronal	Human neuronal	Human ne	Drosophi	Human ne	Alpha 2	Neuronal	Human ne	Human ne	Prostate	Caenorhabditis	Caenorhabditis		Modified	Modified	Neuronal	Drosophila	Drosophila
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AAB50012	ABB82435	ABG70492	AAW69216	AAW12368	AAB50015	AAB50016	AAB50017	AAW12369	AAE12824	ABP96318	AAW09022	AAB50014	ABB82431	ABG70488	ABB61954	AAB50018	AAW44156	AAW09018	ABB82434	ABG70491	ABB62727	AAW44155	AAR73966	AAW09021	ABB82430	ABG31800	ABG61850	AAE12823	ABP96317	AA017243	AA017245	ABB08885	AAR07143	ABB62694	ABB61667
22	23	23	19	18	22	22	22	18	22	24	18	22	23	23	22	22	15	18	23	23	22	15	16	18	23	23	23	22	24	23	23	23	11	22	22
502	. 502	502	502	502	502	502	502	511	554	554	504	470	504	504	216	448	504	464	464	464	580	529	529	529	529	529	529	479	479	631	622	622	495	519	552
47.7	47.7	47.7	47.5	47.5	47.4	47.3	47.1	46.5	40.9	0	37.5	36.5	δ.	35.9	35.7	S	35.6	35.3	5.	ъ.	δ.	-:	4.	34.9		4	٠	7	₹.	34.8	34.7	34.7	34.5	34.4	34.3
1258.5	1258.5	1258.5	1254.5	1253	ď	m.	1242.5	'n	98	1080	989.5	962.5	946.5	946.5	943	942		3	933	3	93	922.5	22.	22.	22.	22.	922.5	922	92	918.5	915	7	910.5	<u>.</u>	906
. 10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	. 25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RES	RESULT 1	
AAY	AAY50816	-
Ω	AAY50816 standard; Protein;	in; 501 AA.
XX		
AC	AAY50816;	
XX		
DT	17-FEB-2000 (first entry)	(A)
×		•
DE	H. virescens acetyl-chol	H. virescens acetyl-choline receptor protein from clone Hva7-2.
XX	•	•
ΚW	Acetyl-choline receptor;	Acetyl-choline receptor; nicotinic; insect; insecticide; screening
Κ¥	neurotransmission; plant	neurotransmission; plant protection agent; conductance; AChR.
X		
SO	Heliothis virescens.	
XX		
PN	DE19819829-A1.	
×		
PD	11-NOV-1999.	
×		
ÞΕ	04-MAY-1998; 98DE-1019829	829.
X		_
PR	04-MAY-1998; 98DE-1019829.	829.
××		
PA	(FARB) BAYER AG.	
XX		
ΡI	Adamczewski M, Oellers N,	N, Schulte T;
XX		
DR	WPI; 2000-014207/02.	
DR	N-PSDB; AAZ24477.	
XX		
ΡŢ	New nucleic acid encoding	New nucleic acid encoding a nicotinic acetylcholine receptor from
ΡŢ	insects, used to identify	y potential insecticides -

Schulte

Oellers N,

98DE-1019829 98DE-1019829

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New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides \,
                                                                                                                             2000-014207/02.
                                                                                                                              WPI; 2000-014207/
N-PSDB; AAZ24476.
                                                                                                       Adamczewski M,
DE19819829-A1
                                                                                   (FARB ) BAYER
                                         04-MAY-1998;
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                           This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved formation of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
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                                                                                                                                                                                                                                                                                                             GTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H. vicescens acetyl-choline receptor protein from clone Hva7-1
                                                                                                                                                                                 DB 21; Length 501;
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                                                                                                                                                                                                      Indels
                                                                                                                                                                                100.0%; Score 2640; DB 21;
100.0%; Pred. No. 5.8e-270;
ive 0; Mismatches 0;
          Page 22-23; 26pp; German.
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                                                                                                                                                            501 AA;
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSTMEDVGGGLGSH-----HRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                              68:3%; Score 1803.5; DB 21; Length 496; 68.7%; Pred. No. 1.9e-181; ive 53; Mismatches 78; Indels 27;
                                                                                                                                                                                                                                                                                                                     recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
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Example 1a; Page 17-19; 26pp; German
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Matches 347; Conservative
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617 413

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414 FRRSFVRPSTMEDVG--GGLGS------HHR------ELHLILRELQFITARMKKA 455
                                                                                                                                                                                -----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS
                                                                                                                 SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG-----GTLPHNPAFYRTV
                                SSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRK - - - TIMMNTR
                                                                                              363 -----MRELELKERSSKSLLANVLDIDDDFRHG--PPPPNSTASTGNLGPGCSIFRTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
535 SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---
                                                                                                                                                                                                                                                 DEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHIIV 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 8088
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11-JUL-2000; 2000US-0614150.
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Matches 319; Conservative
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pharmaceutical.
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interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LLALLPVSEQ----GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                            Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.;
                                                                                                                                                            D. melanogaster acetyl-choline receptor protein from clone Da7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.9%; Score 1609; DB 21; 60.8%; Pred. No. 1.4e-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Schulte T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1a; Page 12-14; 26pp; German
                                                             AAY50814 standard; Protein; 770 AA.
                                                                                                                                                                                                                                                                                                                                                                             98DE-1019829.
                                                                                                                                                                                                                                                                                                                                              98DE-1019829.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Oellers N,
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 60.8
Matches 319; Conservative
                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-014207/02.
N-PSDB; AAZ24475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Adamczewski M,
                                                                                                                                                                                                                                                                           DE19819829-A1.
                                                                                                                                                                                                                                                                                                                                            04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                             04-MAY-1998;
                                                                                                                                                                                                                                                                                                            11-NOV-1999.
                                                                                                                             17-FEB-2000
                                                                                              AAY50814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                             RESULT 3
                                              AAY5081
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.. و is The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. ed nucleic acid detection reagent for detecting 1000 or more Drosophila and for elucidating cell signalling and cell-cell The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10176-ABL30511), expressed DNA sequences (ABL01875) and the encoded proteins. Gaps Length 498; 75; Disclosure; SEQ ID NO 8088; 21pp + Sequence Listing; English. 84; Indels 59.5%; Score 1570.5; DB 22; 61.1%; Pred. No. 8.6e-157; iive 44; Mismatches 84; In

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                        20 LVYGLGLLIMIPACAAGPHEKRLHAALLDNYNSLERPVVNESDPLQLSFGLTLMQIIDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 ATNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDEA
                                                                                                                                                                                                                                                                                                                                      4 MLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVD
                                                                                                                                                                                                                                                                                                                                                                                                       EKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTY
                                                                                                                                                                                                                                                                                                                                                                                                                       QTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVL
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor; alpha-7 subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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Disclosure; SEQ ID NO 17841; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                    Length 311;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                      48.6%; Score 1283; DB 22;
79.4%; Pred. No. 1.1e-126;
79.4%; Vienatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229..256
/label= TMD1
/note= "transmembrane domain"
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/note= "transmembrane domain"
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/note= "transmembrane domain"
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/label= TMD4
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; neuronal nicotinic acetylcholine Drain tissue; screening; NAChR; antibody
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'label= signal
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                                                                                                                                                                                                                                                                                     al Similarity 79.4
231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 284
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                                                                                                                                   sequences (ABL01840 (ABB57737-ABB72072)
                                                                                                                                                                                                                                      311 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1998
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                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                     Query Match
Best Local 3
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                                                                                                  SKSLLANVLDIDDDFRH------TISGSQTAIGSS-----ASFGRPTTVEEHHTAIG 456
                                                                                                                                                 DEGFDGTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQL 175
                                                                                                                                                                                                                    221
                                                                                                                                                                                                                                                                                                                     291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                -----ILFFQFNCAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKPCRRVH
                               DLVLKDEAGGDLSDFITNGEWYLIGM-PGKKNTITYACCP-------EPYVDVT
                                                                                                                                                                                                                                      ------TILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTV
                                                                                                                                                                                                                                                                                                                                                                        292 ADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQC-RAESTYFNCIMFMVASSVVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                       VVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMRELELKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVRPSTMEDVGGGLG
                                                                               LQQIIDVDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                     FTIMIRRRILYYFFNLIVPCVLISSMALL----GFTLPPDSGEKLTLGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHREDELLILKELQFITARMRKADDEAELIGDWRFAAMVVDR 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDR 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
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ABB63683 RESULT

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G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408 SIFRTDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acetylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also ART48239). Host recombinant alpha-7 subunit, opt. in combination with other recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunits (see also AAW09018-24, AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity.
                                                                                                                                                                                                                                                                                                                                                                                                   nicotinic acetylcholine receptor; nAChR; neurotransmitter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acids encoding nicotinic acetylcholine receptor sub-units screening to determine the effect of drugs on the receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                            Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138; Indels
                                                                                                  KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                       47.7%; Score 1258.5; DB
48.6%; Pred. No. 9e-124;
tive 75; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 73-74; 108pp; English.
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                                                                                                                                                                                                                                        AAW09025 standard; Protein; 502
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                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                     ligand-gated receptor
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Matches 250; Conserv
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                                                                                                                                                                                                                                                                                                                      09-APR-1997
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                                                                                                                                                                                                                                                                               AAW09025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta MAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits on specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer that are saide effects that drugs identified e.g. screening with cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                        Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. Which modulate activity of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.7%; Score 1258.5; DB
48.6%; Pred. No. 9e-124;
tive 75; Mismatches 13
                                                                                                                                                                                                                    INST BIOTECHNOLOGY IND ASSOC
318..461
/label= cytoplasmic_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 80-81; 99pp; English.
                                                                                                                                                                                                                                                                               Harpold MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that express a variety of subtypes
                                                                                                                                                                                                                  (SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                       94WO-US02447
                                                                                                                                                                          93US-0028031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                           Elliott KJ, Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                  WPI; 1994-303024/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              502 AA
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                                                         WO9420617-A2
                                                                                                                                   38-MAR-1994;
                                                                                                                                                                          38-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250;
                                                                                                15-SEP-1994
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                                                     ISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLISA 246
                                        MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
                                                                                            SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366
                                                                                                                     SVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHKQRRCSL 366
                                                                                                                                                  407
                                                                                                                                                                           ------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 407
                                                                                                                                                                                                       SIFRTDFRRSFVRPSTMEDV - -GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour; diagnosis; neoplastic disease; neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferation; tumourigenesis; identification; cancer; cytostatic; concortopic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; anglogenic; hypothalanic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; macrophagal disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides encoding PRO polypeptides, useful in the diagnosis and prevention of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillan KJ,
ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL----
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                                                                                                                                                                                                                                                         466 KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                                                                                          Human PRO2145 protein sequence SEQ ID NO:77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 61; Fig 58; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                      AAB24088 standard; Protein; 502
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99WO-US30911.
2000WO-US00219.
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99WO-US12252.
99US-0141037.
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Wood WI;
                                                                                                                                                                            367 ASVEMSAVA----
                                                                                                          (GETH ) GENENTECH INC
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N-PSDB; AAC58395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-2000;
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20-DEC-1999
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treatment,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 SIFRTDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G------RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460
                                                                                                                                                                                         PRO genes. Exemplary conditions or disorders to be treated with supplications or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kindrey, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vurious head and neck tumours) leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC5836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC5836 and AAC5836 represent human PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GPGC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASVEMSAVA--------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
            one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO6199, PRO8109, PRO8109, PRO8109, PRO8109, PRO8109, PRO8109, PRO8109, PRO8109, PRO1025, PRO1029, PRO1030, PRO1030, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187, PRO1281, PRO23, PRO39, PRO814, PRO1111, PRO1153, PRO2094, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO PRO1069 and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including
                                                                                                                                                                                 those characterised by overexpression and/or activation of the amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 9e-124;
75; Mismatches 138; Indels
present invention describes an isolated antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL----
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intervene in neuronal signalling pathways, especially where the ligand-gated ion channel is the nAChR, and the related disorder Tourette's syndrome, Alzheimer's disease, addiction to nicotine or schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    been substituted. New drugs can be developed that selectively
                                                                                                                                                                                                                                                                                              Disclosure; Page 252-254; 260pp; English.
             Nicotinic acetylcholine receptor alpha7.
                                                                                                                                                                                                                         (TEWE-) STICHTING TECH WETENSCHAPPEN,
                                                                                   Location/Qualifiers
                                                                                                                                                                                         09-FEB-2001; 2001WO-EP01457.
                                                                                                                                                                                                      2000EP-0200443
                                                                                                                                                                                                            2000EP-0203810
(first entry)
                                                                                                            171..173
                                                                                                                               210..217
                                                                                                                                                                                                                                                  WPI; 2001-497071/54
                                                                                                                                                                                                                                      Sixma TK;
                                                                                                                                                               WO200158951-A2
                                                                                                                                                                                                                                                                                   schizophrenia
                                                                                                                                                                                                    10-FEB-2000;
                                                                                                                                                                                                             31-OCT-2000;
15-0CT-2001
                                                                      Homo sapiens
                                                                                                                                                                            16-AUG-2001
                                                                                                                                                                                                                                      Smit AB,
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χχ g qq £ ŏ g ò ŏ g qq g à qq g à 셤 ŏ ò δ ŏ Water-soluble ligand-binding proteins derived from molluscs and analogue of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or The present sequence is that of the alpha subunit of human nicotinic acetylcholine receptor (nAChR). The sequence includes regions that are conserved throughout the various nAChR alpha subunits and which are essential for ligand binding. The invention relates to water soluble ligand-binding proteins derived from analogues of ligand-gated ion channels, their crystals, and their use for screening ligands of ligand-gated ion channels. The water-soluble ligand-binding proteins are capable of forming use for screening ligands of ligand-gated ion channels. The water-soluble ligand-binding proteins are capable of forming unlimers and are amenable to crystallization. The crystal cructure of AChBP is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated in channels and thus for screening of drugs that act on these /note= "conserved ligand-binding region, residues Tyr210, Cys212, Cys213 and Tyr217 are essential" ion channels. Chimeric proteins are provided that are capable of bloding a ligand gated receptor, and comprise at least the amino acids of the AChBP determining solubility of the AChBP, in the same positions as in the AChBP, and also comprising amino acids determining binding to the ligand. In the chimeric proteins, at least the essential amino acids of at least 1 of the conserved regions of an nAChR have been substituted for the corresponding amino acids, and preferably entire stretches have /note = "conserved ligand-binding region, residues residues Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; duug design; protein co-ordinate data; schizophrenia; Alzheimer si disease; nicotine addiction; Tourette's syndrome; therapy; nootropic; neuroprotective. /note= "conserved.ligand-binding region, Trp171 and Tyr173 are essential Trp108 and Tyr115 are essential

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                                                                                                   10 LALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN
                                                                                                                                               67 QLLITNIWLŞLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
                                                                                                                                                             127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                                                                                                    LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
                                                                                                                                                                                                                                                                                   MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 ASVEMSAVA-------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 SIFRIDERRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                                                                                                                                                                        SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
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                                                         51; Gaps
                           Length 502;
                           47.7%; Score 1258.5; DB 22; Lengt.
48.6%; Pred. No. 9e-124;
live 75; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wild-type human alpha7 ligand gated ion channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-061524/07.
N-PSDB; AAC90380.
                                            Local Similarity
502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200073431-A2.
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                                                         Matches 250;
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 Sequence
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                              Query Match
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2001WO-US50985. 2000US-0703951.

29-OCT-2001;

01-AUG-2002

01-NOV-2000;

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                                                                                                              The present sequence is wild-type human alpha? nicotinic acetylcholine gated ion channel. The human alpha? ion channel was used in the construction of an alpha?/5-hydroxytryptamine (5-FT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha?/5-HT3 chimeric invention, resulting in preferential calcium ion conductance by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASVEMSAVA-------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        screening;
                                                                                                                                                                                                                                                                                                                                                69
          Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH
                                                                                                                                                                                                                                                                                                                                   VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
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ISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLISA
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                                                                                                                                                                                                                                                             Length 502;
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                                                                                                                                                                                                                                                             DB 22;
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KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                           Score 1258.5; DB
Pred. No. 9e-124;
; Mismatches 13
                                                                               Disclosure; Pages 61-63; 77pp; English.
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                                                                                                                                                                                                                                                        47.7%; Scor
48.6%; Pred
tive 75; 1
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                                                                                                                                                                                                                                  502 AA;
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immunochemistry;
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                                                                                                                                                                                                                                                                                                               The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or tibonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The composition and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence.represents a human neuronal NAChR alpha? subunit.
                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVVVTVIVLOYHHDDDGGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHKQRRCSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
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                                                                                                                                                                                                                                 beta subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                           ΚЈ;
                                                                                                                                                                                                                                               neuronal nicotinic acetylcholine receptors, useful for in vitro
screening of a drug substance in a test system specific for humans
                                                                                                                                                           Elliott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 9e-124; 75; Mismatches 138; Indels
                                                                                                                                                           Α,
                                                                                                                                                                                                                                 Cell comprising nucleic acids encoding human alpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL-----
                                                                                                                                                           Siegel
                                                                                                                                                           Chavez-Noriega LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.7%; Score 1258.5; 48.6%; Pred. No. 9e-1
                                                                                                                                                                                                                                                                                          Examples; Page 130-131; 143pp; English.
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                                                                                                                                                           Claeps BO,
                                                                                                                             (MERI ) MERCK & CO INC
                                                                                                                                                                                        2002-698532/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                        N-PSDB; ABV73248
                                                                                                                                                           Gillespie A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250;
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This sequence is the V247T variant of human alpha7 nicotinic acetylcholine receptor (nAChR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 nAChR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic
                                                                                                                                                                                                SVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHKQRRCSL 366
                                                                                                                                                                                                                                                          367 ASVEMSAVA------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 407
                                                                                                                                                                                                                                                                                                                                           G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease;
                      LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
                                                                                          MALLGFTLPPDSGEKLTLGVT1LLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                          SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                                                                                                                                        SIFRIDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                     ---GPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding variant of human alpha? nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the receptor, potentially useful for treating neuro-degeneration, cancer, affective disorders etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McKenna DG, Monteggia LM;
                                                                                                                                                                                                                                  ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL----
                                                                                                                                                                                                                                                                                                                                                                             466 KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                                                                                                                                                                                                                 V274T variant human alpha7 nAChR protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Тоита
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the NAKARR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to
                                                                                                                                                                                                                                                               nicotinic acetylcholine receptor; nNAChR; receptor; 7 subunit.
                                                                                                                                                                                                                              Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
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KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                   494
                Claim 101; Column 59-64; 56pp; English.
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                                                                                                                      ABG70492 standard; Protein; 502
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93US-0028031.
93US-0149503.
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N-PSDB; ABS54875.
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!on flux; alpha
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08-MAR-1993;
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                                                                                                                                                                                                   OLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYOTN 126
                                                                                                                                                                                                                                         VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186
                                                                                                                                                                               69
      psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha? NAChR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
                                                                                                                                                                      MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
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osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
                                                                                                                                                            LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                 SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
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                                                                                                                                         51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic; ligand binding; ion channel.
                                                                                                                     Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                       ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL------
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                                                                                                                                         Indels
                                                                                                                     DB 19;
                                                                                                                    47.5%; Score 1254.5; DB 19, 48.4%; Pred. No. 2.4e-123; ive 75; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
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                                                                                                                              Best Local Similarity 48.4 Matches 249; Conservative
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/label=
                                                                                                 502 AA;
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                   The alphal subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid sequences of chick neuronal alpha-bungarotcoxin binding protein (AABBP) were deduced from newly isolated DNA molecules (AAT59186-97) obtd. from an 18-day chick embryo cDNA library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact ABBP subtypes. The ABBP alphal and alpha2 subunits can also be used to produce subunit peptides for use as immunogens for preparing antibodies to permit affinity purification of subtypes and their histological location.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 APMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 VDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 TYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMRELELKERSSKS----LLANVLDIDDDFR-----HGPPPPNSTASTGNLGPGCSIFRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRCSLSSMEMNTVSGOOCSNGNMLYI - - GFRGLDGVHCTPTTDSGVICGRM - - TCS - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                              New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1253; DB 18;
Pred. No. 3.5e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 AAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                               STUDIES
                                                                                                                                                                                                                                                                                                                                                                  Example; Fig 2A-B; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.5%;
                                                                                             INST BIOLOGICAL
89US-0413947
                                             89US-0413947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 250; Conservative
                                                                                                                                               Lindstrom JM, Schoepfer
                                                                                                                                                                                               WPI; 1997-118297/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 AA;
                                                                                                                                                                                                                        N-PSDB; AAT59196
                                                                                               (SALK ) SALK
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465 407

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408 G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460
    MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                           SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                            408 SIFRTDFRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                           367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL
                                                                                                                                                                                                                                                                                                                                                                                                                 466 KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
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Job time : 45.9474 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a mutant human alpha? nicotinic acetylcholine gated ion channel. The human alpha? ion channel was used in the construction of an alpha?/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha?/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LALAASLIHVSLQGEFQRKIYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bΗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                       Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild-type Thr substituted by Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.4%; Score 1252.5; DB 2
llarity 48.4%; Pred. No. 3.9e-123;
Conservative 75; Mismatches 139;
                                                                                                                                                                                                                                                             Mutant human alpha7 ligand gated ion channel #1.
Claim 100; Pages 70-72; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                  AA
                                                                                                                               AAB50015 standard; Protein; 502
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                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-061524/07.
N-PSDB; AAC90385.
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249; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                  14-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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Best Local s
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Matches
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em_gss_pln:* em_gss_tun:* em_gss_mam:* em_gss_mam:* em_gss_mam:* em_gss_pro:* em_gss_rod:* em_gss_rod:* em_gss_rod:* em_gss_rod:*	<pre>m htc:*</pre>	Database : EST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estin:* 5: em_estov:* 6: em_estpl:*	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Searched: 22781392 seqs, 12152238056 residues Total number of hits satisfying chosen parameters: 45562784	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Title: US-09-303-232-5_COPY_95_1597 Perfect score: 1503 Sequence: 1 atggcccctatgttggcggccaccgcatatcatcgtgcaa 1503	<pre>Run on: August 21, 2003, 03:48:31; Search time 3282.73 Seconds (without alignments) 11127.831 Million cell updates/sec</pre>	OM nucleic - nucleic search, using sw model	GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	BG632919 GH16126.3 AI292581 GH15518.5 AL530299 AL530299 AK034228 Mus muscu
SUMMARIES	c 1 423.8 28.2 885 10 BG632919 2 331.2 22.0 607 9 AL530281 3 301.2 20.0 1201 9 AL530299 4 293.2 19.5 2940 11 AK034228
08	90
% Query Match Length DB ID	885 607 1201 2940
å Query Match	28.2 22.0 20.0 19.5
Score	423.8 331.2 301.2 293.2
esult No.	4321
Result No.	: 0

Mus muscu Mus muscu Mu	Tetracodon 60294157 Drosophil Drosophil Mus muscu Mus muscu Bx299163 Drosophil RST9980 A 602420721
AKO83157 AKO81254 AKO817422 AKO517420 AKO517430 AKO517430 AKO80475 CB245337 AKO80475 CB245337 AKO80475 CB245337 AKO80475 CB149460 AKO31264 BM711715 CB149460 AKO31264 BM711715 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069 CA373069	ALL157677 B1195149 B1195149 AL073676 AK071277 AK010496 AK010496 BG190899 BG404575 BB637693
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3157 11254 112554 17422 17430 117430 117430 117430 12491 12491 1215 12491 1216 1216 1216 1216 1216 1216 1216 12	38TCF 5149 0001F 0017U 0496 0496 0679 06899
AK083157 AK081254 AK081254 AK081972 AK053497 AK080475 AK080475 AK080475 AK080475 AK080475 AK080475 AK080475 AK03124 AW914206 BW733068 BW733068 BW733068 BW733068 BW733068 BW733068 BW733068 BW733068 BW733068 BW733068 BW733069 BW733069 BW733069 BW733069 BW733069 AW0373069 BW733069 AW0373069 AW0373069 BW733069 AW0373069	CNSO2DC CNSO2DC B1195149 CNSO001F CNSO001J AK010496 AK010496 CNSO06F9 BG190899 BG404575
	100 100 100 100 100 100 100 100
3230 3483 4047 4046 1046 11864 12916 2010 908 908 922 1036 1036 1034 1034 458 755 658 759 759 664 763 458 763 458 763 763 763 763 763 763 763 763 763 763	1001 882 1101 1001 1007 3827 1835 586 978 830 830
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8893 1000 1000 1000 1000 1000 1000 1000 10	190.6 188.4 188.2 187.2 186.8 1182.8 1179.6 177.8
2 3 3 3 3 3 6 5 5 5 6 5 6 6 6 6 6 6 6 6 6	0 1 M W W W W A A A A A A 1 N M C M W O O U U W A N

ALIGNMENTS

RESULT 1 BG632919/C LOCUS DEFINITION ACCESSION VENESION	BG632919 GH16126.3prime GH Drosophila melanogaster head por 2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128 bG632919 GG532919 I GI:13758409
SOURCE	Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptery Endoptery pota; Diptery achieva; Muscomorpha; Enhydroidea: Drosophilidae: Drosophila
REFERENCE AUTHORS TITLE JOHRNAL	1 (bases 1 to 885) Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G. M. BDGP/HMI Drosophila EST Project
COMMENT	Other_ESTS: GH16126.Sprime Contact: Stapleton, M. BDGP Lawrence Berkeley National Lab
	One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Based upon the presence of a XhoI site followed by a run of 14 or

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more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AE0013511. arm:X [18792641,19136447] estimated-cyto:18A3-18C6: 04/10/2001 plate: GH.IGI row: C column: 2 High quality sequence stop: 784.
                                                                                                                                /db_xref="taxon;727"
/clone="GH16126"
/sex="male and female"
/sex="male and female"
/sex="male and female"
/lab_host="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cONAs were directly ligated into
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                      825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAGGACCTCAGGATCACGCCCCAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCTGACGAGGGTTTTGACGGGACCTACCAGACCAACGTGGTGGTCAGAAGCGGCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGTCTGTACGTACCGCCAGGTATATTTAAGTCAACGTGTAAGATCGACATTACGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTCAACCTGATCGTCCCGTGCGTGCTGATCTCATCGATGGCACTCCTCGGCTTCACAC
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                                                                                                                                                                                                                                                                                                                                                                                                               GCCTGTCGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACAGCGAGTATGGCGGGG
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                                                                                                                                                                                                                                                                                                      Length 885;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                            1. .885
/organism="Drosophila melanogaster"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                     Score 423.8; DB 10;
Pred. No. 2.2e-106;
); Mismatches 262;
                                                                                                                                                                                                                                                  cDNA library."
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68.9%;
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GG15518.5prime GH Drosophila melanogaster head port2 Drosophila melanogaster head port3 Brosophila melanogaster construction GG15518.5prime GH Drosophila similar to CG4128: FBan0004128 (ion channel' located on: 2L 3001-3061; 04/10/2001, mRNA sequence.
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/lab_host="pHS - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/clone_lorgan: head vector: pOT2; Site_l: EcoRI; Site_2:
/hot="Corgan: head vector: pOT2; Site_l: EcoRI; Site_2:
/hots: Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
                    941 TACTCAATTACCACCATCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAG
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Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic ABC003626: arm:2L [9617316, 9882551]
estImatel-cyto:30C7-30F4: 04/10/2001
Plate: GH.155 row: B column: 6
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 607)
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Pred. No. 1e-80;
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Contact: Stapleton, M.
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Drosophila melanogaster
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al Similarity 76.7%;
405; Conservative
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Qy 131 Db 195	AGAGCGAACCGCTAGAGGTTCGGCTTGACCTTGCAGCAAATCATGACGTGGACG 190 	Query Match Best Local Matches 53	/ Match Local Similarity Nes 537; Conse
Oy 191 Db 255	AGAAGAATCAACTTATAACCAATATATGGCTGTCGTTGGAGTGGAATGACTACAACC 250 	Qy Db	65 ACGAGAAG : 197 WCCAGAGG
Qy 251 Db 315	TGAGGTGGAACGACAGGGGTATGGCGGGGTCAAGGACCTCAGGATCACGCCCAACAAGT 310 	QY Db	125 CCAACGAG
Oy 311 Db 375			185 TGGACGAGA 317 TGGATGAGA
Oy . 371 Db 435		. yo a	
Oy 431 Db 495	AGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCAACACTGTGATATGA 490 	do do	305 ACAAGTTG' 437 GCCAGATT'
Oy 491 Db 555	AGTICGGTAGCIGGACATATGACGGCAATCAGTIGGATCTGGTGCIAA 538 	da	365 CCTACCAGA 1 1 1 497 CATTCCACA
RESULT 3 AL530299		oys.	425 TATTCAAG
z _	AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens CDNA clone CSODD007YP05 5-PRIME, mRNA sequence. AL530299.2 GI:31068132	o ko d	
	ESI. Homo sapiens (human) Homo sapiens	QY Db	545 AGGCAGGC 675G
EU Ma REFERENCE 1 AUTHORS LA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201) 11, W B Griber C Jacob I and Dolawae D	δ t	605 CAGGCAAA
	Full-length cDNA libraries and normalization Unpublished On Feb 13, 2001 this sequence version replaced q::12793792.	άδ	
S 9 9 9 9 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8		qa ko qa	788 TCACAGTGA 725 TGCTGATCA 1111 111
d1 76 76 76	St 2	, ooy	
nt Fa FaTURES Source	<pre>tcp://rulllength.invitrogen.com/ InVitroGen Corporation 1600 araday Avenue Genoscope sequence ID : CS0DD007CH03QP1. Location/Qualifiers 11201</pre>	QY Db	
	/organism="Homo sapiens" /mol_type="mRNH" /db_xref="taxon:9606" /clone="CSODD007xP05" /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED" /clone_llb="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was	Oy Db RESULT 4 AK034228 LOCUS	903 GTTCATGG7 1028 GATCATCG7 AK034228
BASE COUNT ORIGIN	digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized." 258 a 326 c 319 g 273 t 25 others	DEFINITION ACCESSION VERSION	N Mus musculu enriched li nicotinic, AK034228

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2940 bp mRNA linear HTC 05-DEC-2002 llus adult male diencephalon CDNA, RIKEN full-length library, clone:9330165116 product:cholinergic receptor, alpha polypeptide 4, full insert sequence.
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                                                               GAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGG
                                                                               STGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGA
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   Length 1201;
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20.0%; Score 301.2; DB 9; 60.2%; Pred. No. 3e-72; ive 10; Mismatches 333;
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Riken

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Direct Submission
Submitted (16-JUJ-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group KIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="diencephalon"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MEIGGSGAPPPLLLLPLLLLGTGLLPASSHIETRAHAEBRLLK
RLFSGYNKWSRPVANISDVVLVRFGLSIAQLIDVDEKNQMMTTNVWVKQEWHDYKLRW
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TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSEGGEK
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TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLWMFIIVCLLGTVGLFLPPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AGAGCGAACCGCTAGAGGTCAGGTTCGGCTTGACCTTGCAGCAAATCATTGACGTGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note:"unnamed protein product; cholinergic recepnication; alpha polypeptide 4 (MGD|MG1:87888, GB|NM_015730, evidence: BLASIN, 99%, match-1946)
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Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                        URL: http://genome.gsc.riken.go.jp/, rel:81-45-503-9222
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Pred. No. 7.4e-70;
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/db_xref="taxon:10090"
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/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="G1:26329799"
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55.9%;
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full:length cDRAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2940)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
                                                                                                                           Sciurognathi; Muridae; Murinae; Mus.
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Nature 409 (6821), 685-690 (2001)
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Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                  Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cD
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Sciurognathi; Muridae; Murinae; Mus
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,R., Iregami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Sequencing pipeline with 384 multicapillary sequencer sequencer analysis (RISA) system--384-format AE Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of forth full-length cDNAs

Nature 420, 563-573 (2002)

E (Dases I to 3230)

E (Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kayas, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Okazoki, Y., Satio, R., Satio, H., Saklo, C., Sakai, K., Sakazume, N., Sano, H., Sakazume, N., Sakazume, N., Sano, H., Sakazume, N., Sakazume, N., Sakazume, N., Sano, H., Sakazume, T., Tanaka, 
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SCS), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
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Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,

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AKO81254

Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030030P04 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
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Sciurognathi; Muridae; Murinae; Mus
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                                     454 TAACCAAAGCCCACCTGTTCTATGATGGGCGTGTGCAGTGGACACCCCCGGCCATCTATA
                                                                             AGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCAACACTGTGATATGA
                                                                                                  491 AGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTGCTAAAAGATGAGGCAG
                                                                                                                                                                                  GCGGCGATCTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCA
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High-efficiency. full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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1111 TCATGAAGCGCCCA 1124
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SSCSIDVTFFPFDQQNCTMKFGSWTYDKAKIDLVSMHSRVDQLDFWESGEWVIVDAVG,
TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSECGEK
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RSPRTHTMPAMVRRVFLDIVPRLLFMKRPSVVKDNCRRLIESMHKMANAPRFWPEPES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHPPNSSGAPVLIKARSLSVQHVPSSQEAAEGSIRCRSRSIQYCVSQDGAASLTESK
PTGSPASLKTRPSQLPVSDQTSPCKCTCKEPSPVSPITVLKAGGTKAPPQHLPLSPAL
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                                                          Research Group in Riken
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            Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gcc.riken.go.jp/.

URL:http://fantom.gcc.riken.go.jp/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor,
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Pred. No. 7.8e-70;
0; Mismatches 453; Indels 3;
JRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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/db_xref="taxon:10090"
/clone="C630019M18"
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    .3230
    /organism="Mus musculus"

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Best Local Similarity 55.9
Matches 578; Conservative
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                                                                                                                                                                              /mol_type="mrna"
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                    URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                 1. .3483
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Alzawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Alzawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischman,W., Gasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuch),P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Ring,B., Ringwald,M., Rodiguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishili, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium and the RIKEN Genome Exploration Research
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Genome Res. 10 (10), 1617-1630 (2000) 20499374
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Bono, H., Carninci, P.,

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L Nature 420, 563-573 (2002)

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S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furunco, M., Hangaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horit, F., Imotani, K., 1shii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nokawa, T., Makawa, T., Makawa, T., Makawi, S., Muncara, M., Nomura, K., Numazaki, A., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sopabe, Y., Taqami, M., Taqawa, A., Takahashi, F., Takaku-Akahira, S., Takamasu, M., and Hayashizaki, Y., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Direct, Submission
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PASMQGLAGAFQAEPAAAGLGRSMGPCSCGLREAVDGVRFIADHMRSEDDDQSVREDW
KYVAMVIDRLFLWIFVFVCVFGTIGMFLQPLFQNTTATTFLHSDHSAPSSK"
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TVFLLLISKIVPPTSLDVPLVGKYLMFTMVLVTFSIVTSVCVLNVHHRSPTTHTMAPW
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
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/protein_id="BAC33893.1"
/db_xref="K1-26340460"
/translation="MARCSNSMALLFSFGLIWLCSGVLGTDTEERLVEHLLDPSRYNK
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KKVRLPSKHIWLPDVVLYNNADGMYEVSFYSNAVVSYDGSIFWLPPAIYKSACKIEVK
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                                                                                                                                                                                                                                                                                                                                                                Analysis of the mouse transcriptome based on functional annotation of 60,770~\mathrm{full}\text{-length} cDNAs
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Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H. Toyo-oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
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nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASIN, 99%, match=1498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Division of Experimental Animal Research in Riken contributed to
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Encyclopedia Project of Genome Exploration Research Group in R:
Genomic Sciences Center and Genome Science Laboratory in RIKEN
                                                                                                                      Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Please visit our web site for further details.
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/db_xref="taxon:10090"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                   1154 TGTGCTCAATGTGCACCACCGTTCGCCTACCACGCACACCATGGCGCCCTGGGTCAAGGT 1213
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AK049722.1 GI:26340459
HTC; CAP trapper.
Mus miscull.
                                                                                                                                939 GGTACTCAATTACCACCATCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATC
      GGTGTTCCTCAACCTGGTAGCCGAGACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                         339 TAGTGCTGACGAGGGTTTTGACGGGACCTACCAGACCAACGTGGTGGTCAGAAGCGGCGG 398
                                                                                                                                                                                                                                                                                                                     621
                                                                                                                                                                                                                                                                                                                                               CAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACATGCAAGATGGACATCGCGTG 458
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                                                        CTACAACACCCTGGAGCGACCGTGGCCAACGAGAGCGAACCGCTAGAGGTCAGGTTCGG
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Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Salto, Y., Okazaki, Y., Gojobori, T., Bondo, S., Yamanaka, I., Kadota, K., Matsuda, H., Ashurner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuchi, P., Levis, S., Matsuo, Y., Nikaido, I., Pesole, G., Ouackenbush, J., Schrim, L.M., Staubli, F., Bruki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bolunga, N., Fletcher, C., Fujitch, M., Gariboldi, M., Gustincich, S., Hill, D., Fletcher, C., Fujitch, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, M., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Whashizaki, Y., Soshida, K., Hassegawa, Y., Kawaji, H., Kohtsuki, S.
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130070121 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence. AK051742
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)
6 (bases 1 to 4046).

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanaqaki,T., Haraka,A. Hashizume,W.,

Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,

Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,

Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
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Mus musculus (house mouse)
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Mus musculus 0 day neonate eyeball cDNa, RIKEN full-length enriched library, clone:El30103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
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                                                                                                                                                                                                                                        Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, RRI:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Szoloration Research Group in Riken Division of Experimental Animal Research in Riken contributed to
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/db_xref="G1:26342174"
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Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinaqawa, A., Shiraki, T., Sogabe, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
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nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASIN, 99%, match=1498)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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/strain="c57BL/6J"
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/db_xref="taxon:10090"
/clone="p13070121"
/tissue_type="spinal ganglion"
/clone_lib="RIKEN full-length enr:/dev_stage="12 days embryo"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L. Mature 420, 563-573 (2002)

6 (bases 1 to 1864)

7 Adachi, ., Alzawa, K., Akimura, T., Hara, A., Hashizume, W., Hayashida, K., Hayasu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, P., Kouda, M., Kaya, S., Kurihara, C., Matsuyama, T., Makamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaito, R., Saltoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Tagami, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takaku-Akahira, S., Takaku-Akahira, Y., Tagami, M., Tagawa, A., Taya, T., Yasunishi, A., Takahashi, F., Takaku-Akahira, S., Tay
prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamcto,R., Matsumoto,H., Sakayuchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahkii,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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PETYQDITWRKEGWSYDKAK TDLVLICASMMILKDVWESGEMATIKAPCYKHEIKYNCC
EETYQDITYSLYIRFLLEYTULNITPCLLISFLYULYFLBSDCGRKYLCISVLLS
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/dev_stage="0 day neonate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497)
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0; Mismatches 469;
                                                                                                                                                                                                                 /db_xref="FANTOM_DB:E130103E14"
/db_xref="taxon:10090"
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/qualifiers
1. .1864
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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E Adachi, J. Aizawa, K. Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Haramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakai, Y., Salto, R., Satito, R., Sat
rujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKBN integrated sequence analysis (RISA) system-1384-format Sequencing pipeline with 384 multicapillary sequencer 200138.
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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                   TGATATGAAGTTCGGTAGCTGGACATATGACGCCAATCAGTTGGATCTGGTGCTAAAAGA
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK080415

3126 bp mRNA linear HTC 05-DEC-2002
MUS musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:47300/0744 product:NEURONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                                                                                                                                     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegani,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer 20530913
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                                                                                                                                GTACTCGCTATACATTCGCCGCCTGCTGTTCTACACCATCAACCTCATCATTCCGTG
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                                                       787 CCCGGGCTACAAACATGAAATCAAGTACAACTGCTGTGAGGAGATCTACCAAGACATCAC
                                                                                             CTTCACCATCATGATAAGAAGACGAACCTTGTACTACTTCTTCAACCTGATCGTCCCGTG
                     GCCAGGCAAAAAGAACACAATAACATACGCGTGCTGCCCCGAGCCCTACGTGGACGTCAC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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MRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYF
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EEIYQDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYLPSDGGEKVTLCISVLLS
LTVFLLVITETIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNVHYRTPTHTMPT
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DGTCGYCHHRRYKISNFSANLTRSSSSESVDAYLSLSALSPEIKEAIGSYKYIAENMK
AQNVAKEIQDDMKYVAMVIDRIFLWVFILVCILGTAGLFLQPLMARDDT"
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                                                                                           CACCATGAAGTTCGGCTCCTGGTCCTACGACAAGGCAAAGATCGACCTGGTCCTCA---T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 275.6; DB 1. Pred. No. 5.8e-65;
/db_xref="FANTOM_DB:D130068A06"
/db_xref="taxon:10090"
/clone="D130068A06"
                                                       /tissue_type="spinal ganglion"/clone_lib="RIKEN full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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2916
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SVLLSLTVEPLLVITETIPSTSLVIPLIGEYLLFTMIFVTLSVYTVPYTWHYRYPTT
HYMFWYKAVFLNLLPRVMFMTPPTSTEEDAPKTNFYGAELSNLNCFSRADSKSCKE
GYPCODGTCGYCHHRYKISHRSANITRSSSBSVDAVLSLSALSPETKEALOSVKYI
AENMKAQNVAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFLQPLMARDDT"
                                                                                                                                                                                                                                                                          YNEIIRPVANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWKPSDY
QGVEFMRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKI
DVTYFPFDYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEI
                                                                                                                                                                                                                                         /translation="MRSSDMGVVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFED
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ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497) putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 TCACGAGAAGAGTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGT
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Pred. No. 6e-65;
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                                                                                                                                                         /protein_id="BAC37909.1"
/db_xref="GI:26348539"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="putative"
3126
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                                                                                                                    /codon_start=1
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54.7%;
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                                                                                                        Araway, T. Hara, A. Fukunishi, Y. Konno, H. Adachi, J. Fukuda, S. Aizawa, T. Izawa, M. Nishi, K. Kiyosawa, H. Kondo, S. Yamanaka, I. Saito, T. Izawa, M. Nishi, K. Kiyosawa, H. Kondo, S. Yamanaka, I. Saito, T. Okazawi, T. Saito, T. Saito, T. Saito, R. Kadota, K. Matsuda, H. Ashburner, M. Batalov, S. Casawant, T. Fleischmann, W. Gaasterland, T. Gissi, C. King, B. Kochiwa, H., Kuehl, P. Lewis, S. Matsuo, Y. Nikaido, T. Pesole, G. Quackenbush, J. Schriml, L.M. Staubli, F. Puruno, M. Aono, H. Wagner, L. Washio, T. Sakai, K. Okido, T. Furuno, M. Aono, H. Baldarelli, R. Barsh, G. Blake, J. Boffelli, D. Bojunga, N. Carninci, P. Ge Bonaldo, M. F. Brownstein, M. J. Bult, C. Fletcher, C. Fujita, M. Garlboldi, M. Gustincich, S. Hill, D. Hofmann, M. Hume, D.A. Kamiya, M. Lee, N. H. Lyons, P. Nordone, P. King, B. Ringwald, M. Rodriguez, I. Sakamoto, N. Sasaki, H. Toyo-oka, K. Wandy, R. Weitz, C. Whittaker, C. Wilming, L. Wynshaw-Boris, A. Yoshida, K. Hasegawa, Y. Kach, K. Wand, K. Kasayawa, Y. Kach, K. Wand, K. Kasayawa, Y. Kach, K. Wand, K. Hasegawa, Y. Kach, K. Wand, K. Hasegawa, Y. Kach, Wand, K. Kanda, Y. Kach, K. Wand, K. Hasegawa, Y. Kach, K. Wand, Y. Kach, Y. Ka
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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Fax:81-45-503-9216)
                                                                                Shinagawa, A., Shibata, K., Yoshino, M.,
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                            HTC 05-DEC-2002
                                                                                                                                     963 AGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCATG 1022
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Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
                   CGTGCTGATCTCATCGATGGCACTCCTCGGCTTCACACTGCCACCAGACTCCGGAGAGAA 782
                                                               CCTGCTCATCTCCTTCCTCACTGTGCTCGTCTTCTACCTGCCCTCCGACTGTGGGGGAGAA 963
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                             ACTCACACTTGGAGTCACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCCGA
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Functional annotation of a full-length mouse cDNA collection
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fuvuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hirancho, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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/note="NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3
SUBUNIT (SPTR!AAL58471, evidence: FASTY, 99.8%1D,
100%length, match=1497)
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Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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Matsuo, Y., Nikaido, I., Pesole, G.,
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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295 ATCACGCCCAACAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAATAGTAGTGCTGACGAGGGT 354

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RESULT 13 CB245337

Harada, A.,

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Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T.,
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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4831406G09 product:cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle), full insert sequence.

AK029177
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new grenome Res. 10 (10), 1617-1630 (2000)
ATCCCATCTGAACTCATCTGGAGGCCTGACATCGTCCTCTACAACAACGCGGACGGGAC
                                                421 AGCATGCACAGCCGTGTGGACCAACT---GGACTTCTGGGAAGTGGGGAGTGGCTCATT
                                                                                                                                                                                                                                                                                                                                                                     GACGTCACCTTCACCATCATGATAAGAAGACGAACCTTGTACTACTTCTTCAACCTGATC
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                                 TTTGACGGGACCTACCAGACCAACGTGGTCAGAAGCGGCGGCAGTTGCCTGTACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P. and Hayashizaki, Y.
Idjh-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itch, M., Ishli, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Cojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Rabburner, M., Batalov, S., Casavant, T., Rabota, K., Matsuda, H., Rasukawa, T., Sarito, R., Kuchi, P., Lewis, S., Matsuo, Y., Mikaido, I., Pesole, G., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., Geonaldo, M., Bromstein, M., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, M. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K., Wangi, K., Mangawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y., Yang, Y., Kawaji, H., Kohtsuki, S., And Hayashizaki, Y., Shibata, Y., Kawaji, H., Kohtsuki, S., And Hayashizaki, Y., Shibata, Y., Kawaji, H., Kohtsuki, S., And Hayashizaki, Y., Kawaji, H., Kawaji, H., Kohtsuki, S., And Hayashizaki, Y., Kawaji, H., Kawaji, H., Kohtsuki, S., And Hayashizaki, Y., Kawaji, H., Kawaji, H., Kohtsuki, S., And Hayashizaki, Y., Kawaji, H., Kaw
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

E (bases 1 to 4290)

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E Vatuda, S., Furuno, M., Hangara, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hangara, T., Hiroka, T., Hirokan, T., Hirokan, T., Hirokan, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirokan, T., Kondo, H., Kasuka, T., Katoh, H., Kawai, J., Kojina, Y., Kondo, S., Konno, H., Kasuka, T., Kondo, S., Konno, H., Kasuka, T., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Namura, M., Nishi, K., Namuzaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, R., Shinagawa, A., Shiraki, T., Sasaume, N., Tagawa, A., Takada, Y., Tanaka, T., Tomaru, A., Takada, Y., Tanaka, T., Tomaru, A., Tomaru, A., Toya, T., Yasunishi, A., Hura, S., Haraka, M., Muramatsu, M., Andayashizaki, Y., Tagawa, A., Toya, T., Yasunishi, A., Haraka, T., Polato, E., Maransa, M., Toya, T., Yasunishi, A., Haraka, T., Maransa, M., Maransa, M., Toya, T., Yasunishi, A., Haraka, T., Maransa, M., Maransa, M., Toya, T., Yasunishi, A., Haraka, T., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Haraka, T., Maransa, M., Mara
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Submitted (16-JUJ-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yaneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Haysahizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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Nature 409 (6821), 685-690 (2001)
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Fax:81-45-503-9216)
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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AGENCOURT_8443358 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6192234 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             984 TCGCCCAGCACCCACATCATGCCCGAGTGGGTGCGGAAGGTTTTTATCGACACTATCCCA 1043
                                                                                                                                                                                                                                                                                                                            GAGACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATC 900
                                                                                                                                                                                                                                                                                                                                                       AAACTCACACTTGGAGTCACTATTCTTATCGCTGACGGTGTTCCTCAACCTGGTAGCC 840
                                                                                                                                                                                                                                                                                                                                                                                                                        ATGITCATGGTAGCGTCGTCTGTGGTACTGACTGTGGTGGTACTCAATTACCACCATCGA 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGATGACGCTGAGCATCTCTCTTACTGTCCCTGACCGTGTTCCTTCTGGTCATTGTG 863
624 CGGGGCTGGAAGCACTGGGTGTTCTACTCCTGCTGCCCCACCACTCCCTACCTGGACATC 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_l:
Not1; Site_l: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                            TGCGTGCTGATCTCGATGGCACTCCTCGGCTTCACACTGCCACCAGACTCCGGAGAG
                                                ACCTTCACCATCATGATAAGAAGACGAACCTTGTACTACTTCTTCAACCTGATCGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 908) NIH-WGC http://mgc.nci.nih.gov/. NIH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13593 row. column: 19
High quality sequence stop: 598.
Location/Qualifiers
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:6192234"
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JOURNAL
COMMENT
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BU149265
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/db_xref="G1:36325166"
/db_xref="G1:36325166"
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                                                                                         /tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLVIVELIPSTSSAVPLIGKYMLFTMYFVIASIIITVIVINTHHRSPSTHIMPEWVRK
VFIDTIPNIMFFSTMKRPSRDKQEKRIFTEDIDISDISGKPGPPPMGFHSPLIKHPEV
KSAIEGVKYIAETMKSDQESNNAAEEWKYVAMVMDHILLGVFMLVCLIGTLAVFAGRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACGAGAAGAGCTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGAGACGCGTCTGGTGGCAAAGCTCTTTGAAGACTACAGCAGTGTAGTCCGGCCAGTG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACAACCTGAGGTGGAACGACAGCGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 AACAAGTIGIGGAAGCCGGACGICCIIAIGIAIAAIAGIGCIGACGAGGGIIIIGACGGG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAAAGATCTGGCGCCCGGACGTCGTTCTCTATAACAACGACGCAGCGACTTTGCCATT 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATTCAAGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCAACACTGT 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 GAGGACCACCGTGAGATTGTACAAGTCACCGTGGGTCTACAGCTGATCCAGCTTATCAAT 206
                                                                                                                                                                                       /note="unnamed protein product; cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (MGD|MGI:87885, GB|NM_007389, evidence: BLASTN, 99%, match=1763)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 246.2; DB 11; Length 4290;
Pred. No. 1e-56;
0; Mismatches 438; Indels 6;
  /strain="C57BL/6J"
/db_xref="FANTOM_DB:4831406G09"
/db_xref="taxon:10090"
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/note="putative"
4290
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Best Local Similarity 54.6%;
Matches 535; Conservative
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5'-GACTAGTTCTAGATCGCGAGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Barlor Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies." 21 c 21 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACCAGACCAACGTGGTGGTCAGAAG 392
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                                                                                                                                                                      Gaps
                                                                                                                                                                      10;
                                                                                                                                      Length 908;
                                                                                                                                                                    0; Mismatches 275; Indels
                                                                                                                                      Score 240; DB 13;
Pred. No. 2.7e-55;
                                                                                                                                      16.0%;
60.4%;
                                                                                                                                                    al Similarity 60.4
435; Conservative
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Copyright (c) 1993 - 2003 Compugen Ltd.
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New nucleic acid encoding a nicotinic acetylcholine receptor from

P-PSDB; AAY50816

Neuronal nicotinic

Wild-type human al

1509 1509 1876

Schulte T;

Acceptance of the property of

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                                        This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransanission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens.
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                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                     Sequence 3109 BP; 923 A; 610 C; 742 G; 834 T; 0 other;
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identify potential insecticides
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Pred. No. 0;
); Mismatches
                       Claim 1a; Page 19-22; 26pp; German.
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CTGATCTCATCGATGGCACTCCTCGGCTTCACACTGCCACCAGACTCCGGAGAGAACTC
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cell-cell
                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 575.6; DB 23; Length 1540;
Pred. No. 8.7e-151;
0; Mismatches 394; Indels 135;
                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 genes from Drosophila and for elucidating cell signalling and c
                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 16175; 21pp + Sequence Listing; English.
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23-MAR-2001; 2001WO-US09231
                               2000US-191637P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel nucleic acid (NA) encoding a nicotinic acety1-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) also vectors containing it, its regulatory regions, and antibodies disceted against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acety1-choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACAAGTTGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTTGACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGACGAGAAGAATCAACTAATAACCAATATATGGCTGTCGTTGGAGTGGAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 TACAACCTGAGGTGGAACGACAGCGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 ATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCCACCC
                                                                                              Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3700;
                                                            DNA from clone Hva7-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3700 BP; 893 A; 953 C; 944 G; 910 T; 0 other;
                                                                                                                                                                                                                                       /*tag= a
/product= "acetyl-choline receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 575; DB 21;
Pred. No. 1.9e-150;
0; Mismatches 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor isolated from Heliothus virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schulte T;
                                                            virescens acetyl-choline receptor
                                                                                                                                                                                               Location/Qualiflers
335..1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim la; Page 14-17; 26pp; German.
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llarity 64.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adamczewski M, Oellers N,
                                                                                                                                                           Heliothis virescens.
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                      17-FEB-2000
                                                                                                                                                                                                                                                                                                                                    11-NOV-1999
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727 AGGCGCAAAACGTTGTACTATTTTTCAATCTGATTGTGCCGTGCGTACTGATCGCCTCC 786
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247 CAACTGCTTATAACGAATATTTGGCTCAAATTGGAATGGAACGATATGAATCTTCGATGG 306
                                                                                                                                                                                                                                 CTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAGAAC
                                                                                                                                                                                                                                                                                                                                     ACAATAACATACGCGGGGCCCCGAGCCCTACGTGGACGTCACCTTCACCATCATGATA
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                                                                            CCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACCAGACCAAC
                                                                                                                                            607 ATTTCTAGCTTTATAACCAATGGCGAATGGGACTTGTTAGGTGTGCCCGGTAAACGAAAŤ
                                                                                                                             GTGGTGGTCAGAAGCGGCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACA
                                                                                                                                                                                TGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCAACACTGTGATATGAAGTTCGGT
                                                                                                                                                                                              screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acetyl-choline receptor; nicotinic; insect; insecticide; scree neurotransmission; plant protection agent; conductance; AChR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D. melanogaster acetyl-choline receptor DNA from clone Da7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "acetyl choline receptor."
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372..2684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCTAGAGGTCAGGTTCGGCTTGACCTTGCAGCAAATCATTGACGTGGACGAGAAGAAT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACGAGGGAA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACTACTTATAACCAATATATGGCTGTTGGAGTGGAATGACTACAACCTGAGGTGG 258
(ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed nucleic acid detection reagent for detecting 1000 or more Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                    Drosophila melanogaster expressed polynucleotide SEQ ID NO 35681
                                                                                                                                                                            developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.6%; Score 430.6; DB 23; Length 936; 68.5%; Pred. No. 3.1e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                       Myers
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                                                                           CDNA; 936
                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595; Conservative
                                                                                                                                                                                           pharmaceutical; gene; ss
                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
P-PSDB; ABB69630.
                                                                           ABL13733 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interactions
                                                                                                                           26-MAR-2002
                                                                                                                                                                              Drosophila;
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          1763
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO312, PRO290, PRO341, PRO535, PRO619, PRO311, PRO809, PRO810, PRO8103, PRO10043, PRO1005, PRO1005, PRO1005, PRO1005, PRO1011, PRO1113, PRO1183, PRO1184, PRO1187, PRO1181, PRO1181, PRO1181, PRO1181, PRO1181, PRO3181, P
                                                                          717 CCCGTGCGTGCTGATCTCATCGATGGCACTCCTCGGCTTCACACTGCCACCACGAGTTCCGG
                                                                                                     777 AGAGAAACTCACACTTGGAGTCACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGT
                                                                                                                                                                                                                                2015 rgaaaaarrarcgcrgggrgrraccarcrrgcrcrcgcrgaccgrgrrrcrgaararggr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; neoplastic disease; neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithalial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thirty PRO polynucleotides encoding PRO polypeptides, useful in treatment, diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillan KJ,
                                                                                                                                                                                                                                                                                                                        877
                                                                                                                                                                                                                                                                                          837 AGCCGAGACCCTGCCACAGGTCTCCGACGCTATCCCCCTGT
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99WO-US12252.
99US-0141037.
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99WO-US28313.
99WO-US30911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 50; Fig 57; 286pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe CK,
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20-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTATAATACACTAGAACG 1354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1535 ACCGCCGCATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGATT
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                                                                                                                                                                                                                                         New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 2886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 411.4; DB 21;
Pred. No. 1.3e-104;
); Mismatches 256;
                                                                                                        Schulte T;
                                                                                                                                                                                                                                                                                                                      Claim la; Page 8-12; 26pp; German
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  98DE-1019829
                                                                                                        Adamczewski M, Oellers N,
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nes 565; Conserv
                                                                                                                                                                                     P-PSDB; AAY50814
                                                      (FARB ) BAYER AG
04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1295
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anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified more characterised by overexpression and/or activation of the amplified antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, epital, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastococalic disorders, and inflammatory, angiogenic and immunologic disorders. AACS836 represent pcR primers and hybridisation probes used in the isolation of the human processive control of the companion o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    573 AACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAGAACACAATAACATACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 377.2; DB 21; Length 1509;
Pred. No. 3.6e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 3.6e-95;
0; Mismatches 633; Indels
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                         25.1%;
55.2%;
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                                                                                                                                                                                                                                                                                                                                 present invention.
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5-hydroxytryptamine; 5-HT3; calcium ion conductance;
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ligand-gated receptor; ds.
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                                                                                                                                                                                                                    The present sequence is the coding sequence for wild-type human alpha7 nitochinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells.
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                                                                                                       Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
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                                                                                                                                                                                                                                                                                                                                                                                 Score 374; DB 22;
Pred. No. 2.9e-94;
0; Mismatches 635;
                                                                                                                                                                                      Example 5; Pages 60-61; 77pp; English
                             Æ,
                             Berkenpas
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55.1%;
(PHAA ) PHARMACIA & UPJOHN
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809; Conservative
                            Wolfe ML,
                                                          WPI; 2001-061524/07.
P-PSDB; AAB50012.
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                                             GTGCTGCCCCGAGCCCTACGTGGACGTCACCTTCACCATCATGATAAGAAGACGAACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAATATATGCCTGTCGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACAGCGAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACATGCAAGATGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 ACGCTGGTTTCCCTTTGATGTGCAGCACTGCAACTGAAGTTTGGGTCCTGGTCTTACGG
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                                                                                                                                                                                                                                                                                                                              A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits useful for identifying cpds. that
                                                                                                                                                                                                                                                      Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 374; DB 18; Length 1
Pred. No. 3.2e-94;
0; Mismatches 635; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGCTGGTCCTTGGATCTGCAGATGCAGGA-
                                                                                                                                                                                                                                                                                                  Disclosure; Page 71-73; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                          modulate the activity of human nAChRs
                                                                                                                                               (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.9%;
55.1%;
                                                                                      96WO-US09775
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                                                                                                                                                                               Harpold MM;
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P-PSDB; AAW09025.
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                                                                                                                                                                               ΚЈ,
                            WO9641876-A1
                                                                                   07-JUN-1996;
                                                                                                                   37-JUN-1995;
                                                          27 - DEC - 1996
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This sequence encodes the V247T variant of human alpha7 nicotinic cectylcholine receptor (nAchR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 nAchR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru, psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (inceptor agonists (inceptor agonists).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         but the wild-type inward rectification is
                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAACTACAACACCCTGGAGCGACCGGTGGCCAACGAGAGCGAACCGCTAGAGGTCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGGCTTGACCTTGCAGCAAATCATTGACGTGGACGAGAAGAATCAACTACTTATAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 TCTCCCTGAGCCTCCTGCAGATCATGGACGTGGATGAGAAGAACCAAGTTTTAACCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTGCTGCCCGTATCGGAGCAAGGTCCTCACGAGAAGAGACTCCTGAACGCGTTGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                              therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetyl-choline receptor sub-unit - used to identify modulators of
the receptor, potentially useful for treating neuro-degeneration,
cancer, affective disorders etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19; Length 1590;
           Alpha? nAChR; alpha? nicotinic acetylcholine receptor subunit; neurodegeneration; enzyme dysfunction; affective disorder; then immune dysfunction; diabetic neuropathy; Alzhelmer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         634; Indels
                                                                                                                                                                                                                                                                                                                                                                Monteggia LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding variant of human alpha7 nicotinic
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                  1408 TGGACCGCCTGTGCCTTCTCGGTCTTCACCATCATCTGCATCGCCATCC
                                                    TTGATAGGTTTTGCCTGTTCGTGTTCACACTTTTCACAATCATCGCGACAGTAGCTGTCC
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                                                                                                                                                                                                                                                                  Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.
                                                                                                                                                                                                                                                                                                                                                                                               "neuronal nicotinic acetylcholine receptor alpha-7 subunit"
                                                                                                                                                                                                                                                                                           : neuronal nicotinic acetylcholine receptor; alpha-7 subunit; tissue; screening; NAChR; antibody; ds.
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Length 1876;
   DB 15;
                                  635;
               Pred. No. 4.1e-94;
; Mismatches 635
 Score 373.6;
                                  1;
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55.0%;
                                  Conservative
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Matches 808; Conser
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                                                                                                                                  GAGCGCCGTGGCGCCCCCCCCCCCAGCAACCTGCTGTACATCGGCTTCCGCGG
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                                                                                        GTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTGATGATGACTTCAGACACGGCCC
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The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are subustantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in present sequence represents a human neuronal NAChR alpha7 subunit
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                                                                                                                                                                                                                                                                                  DB. 24;
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08-MAR-1993;
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                                                                                             1005 GGTGATCGTGCTGCAGTACCACCACGACGACGGGGGGGGAAGATGCCCAAGTGGAC 1064
                                                 GTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTGATGATGACTTCAGACACGGCCC
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                                                                                                                                                          1053 GATCACCAGGAAGACTATAATGATGAACACGAGGATGAGGGAGCTGGAACTGAAGGAGAG
                                                                                                                                                                            CAAGGTGCGCCCGGCCTGCCAGCACAAGCAGCGGCGCTGCAGCTGGCCAGTGTGGAGAT
                                                                                                                                                                                                                     GAGCGCCGTGGCGCCGCCGCCGCCACCACGGGAACCTGCTGTACATCGGCTTCCGCGG
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                  TCTTACCGTCTTCATGCTGCTCGTGGCTGAGATCATGCCCGCAACATCCGATTCGGTACC
                                      CCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGGTAGCGTCGTCTGTGGTACTGAC
                                                                             TGTGGTGGTACTCAATTACCACCATCGAACAGCTGATATACATGAAATGCCACAGTGGAT
                                                                                                                    AAAATCAGTATTCCTACAATGGTTGCCATGGATACTGCGAATGTCGAGGCCAGGGAAGAA
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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NNAChRs). By contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic and acid. This sequence represents CDNA encoding the alpha 7 subunit of the
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                                                                                                                                                                                                                                                                                                           agonists of human neuronal nicotinic contacting recombinant cells with test flux of cells or binding of compound to
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                                                                                                                                                                                                                                                                                                              Identifying antagonists or agonists
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                                                                                                                                                                                                                                                                                                                                      acetylcholine receptors, compound, and measuring
                                                                                                                                                                                  SB,
                                                                                                                              S CO INC
                                                                                                                                                                                                                                  2002-711528/77.
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channel; mutant;

Human; alpha7 nicotinic acetylcholine gated ion channel. 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss

МВ;

Berkenpas

WPI; 2001-061524/07

Groppi VE,

(PHAA) PHARMACIA & UPJOHN Wolfe ML,

2000WO-US11862 99US-0136174

25-MAY-2000; 27-MAY-1999;

07-DEC-2000

WO200073431-A2

Homo sapiens

alpha7 ligand gated ion channel

human

Mutant

#1.

coding sequence

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                                                                    CCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGGTAGCGTCGTCTGTGGTACTGAC
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                                                                                                           GTACTACTTCTTCAACCTGATCGTCCCGTGCTGCTGATCTCATCGATGGCACTCCTCGG
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 AACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAGAACACAATAACATACGC
                                                      GTGCTGCCCCGAGCCCTACGTGGACGTCACCTTCACCATCATGATAAGAAGACGAACCTT
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                                                                                                                                                                                                                                                                                          Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH
                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 230 substituted by a proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 TTCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1509;
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AAC90385 standard; cDNA; 1509

RESULT 13 AAC90385 (first entry)

14-MAR-2001

AAC90385

RESULT 14

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            AACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAAGAACACAATAACATACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the coding sequence for a mutant human alpha7 no incottnic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild type cysteine residue at position 241 substituted by a serine
                                                                                                                                                                                                                                                                                                                                                                                                                      Ηđ
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                                                                                                                                                                                                                                                                                                                                                                                       Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
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                                                                                                            Human; alpha7 nicotinic acetylcholine gated ion chann
5-hydroxytryptamine; 5-HT3; calcium ion conductance;
                                                                                human alpha7 ligand gated ion channel coding
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P-PSDB; AAB50017.
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                                                             ACGCTGGTTTCCCTTTGATGTGCACACTGCAAACTGAAGTTTGGGTCCTGGTCTTACGG
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                               342 CTATAACAGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC
                                                   CGGCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACATGCAAGATGGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Special cell culture medium for treating cells and for inducing mammallan cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 230 substituted by a proline residue and the wild-type cysteine residue at position 241 substituted by a serine residue.
GCCGAACTACAACACCCTGGAGCGACCGGTGGCCAACGAGGGAACCGCTAGAGGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; alpha7 nicotinic acetylcholine gated ion channel; mutant; 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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Pred. No. 2.3e-93;
0; Mismatches 637; Indels 24;
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                                                           393 CGGCGCCAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACATGCAAGATGGACAT 452
162 CTTCTCCCTGAGCCTCCTGCAGATCATGGACGTGGATGAGAAGAACCAAGTTTTAACCAC 221
                                     213 CAATATATGGCTGTCGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACGACGAGTA
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129	128	135	133	141	139	147	145	
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Search completed: August 21, 2003, 04:24:43 Job time : 409.032 secs

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OM nucleic - nu	OM nucleic - nucleic search, using sw model	
Run on:	August 21, 2003, 00:04:15; search time 5602.3 Seconds (without alignments) 10975.350 Million cell updates/sec	
Title: Perfect score:	US-09-303-232-5_COPY_95_1597 1503 1 standontstattanna	
Scoring table:	r drycecetarythygryyc	
Searched:	2888711 seqs, 20454813386 residues	
Total number of	Total number of hits satisfying chosen parameters: 5777422	
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing	Post-processing: Minimum Match 0%	

Maximum Match 100%
Listing first 45 summaries

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_pt:*
4: gb_on:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SEPLEWREGITLQQIIDVDEKNQLLITNIMLSLEWNDYNLERNDSEYGGVKDLRITPN
KLWKDWYNNSAGGGCLYVPPGIFKSTCKMDIAMPPEDDQH
CDMKRESWYTDGNQLDLVLKDEAGGBLSDFTYNGEWYLIGMPGKKWTITYACCPEPY
DVYFFTIMIRKTLYYFRNLIYPCVILSSMALLGFTLPPDSGEKLTLGVTLLLSLTVFL
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FLQWLPWILMASRPGKKITRKTIMMYTRMELELKRESSKSLLANVLDIDDDFRHGPP
PPNSTASTGNLGFGCSIFRTDFRRSFVRFSTWEDDWGGLGSHHRELHLILRELQFITA
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                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryg
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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                                                                                                             Adamczewski,M.D., Schulte,T.D. and Oellers,N.D. Nucleic acids encoding acetylcholin-receptor subunits Patent: EP 0962528-A 5 08-DEC-1999;
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/organism="Heliothis virescens"
/mol_type="genomic DNA"
/db_xref="taxon:7102"
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tive 0; Mismatches
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LOCUS E58348 LOCUS E58348 S109 bp DNA linear PAT 18-JUN-2001 DEFINITION Nucleic acid encoding insect actyl choline receptor subunit. ACCESSION E58348 GES348 GES348	Patent: JP 2000023680-A 3 25-JAN-2000; BAYER AG CS Hellothis virescens PN JP 2000023680-A/3 PD 25-JAN-2000 PF 26-JAN-2000 PF 26-JAN-2000 PF 26-MAX-1999 JP 1999118159 PR 04-MAX-1999 DE 19819829.9 PR MARTIN ADAMUTSIEUSUKI, NADJA ERASU THOMAS SCHULTE PC CIZNIS/99, A01K67/033,C07K14/705,C07K16/28,C12N1/21,C12N5/1 C1201/68, PC G01N33/15,G01N33/50//(C12N1/21,C12R1:19),C12N15/00,C1 FH Kev	FH ACY LOCALION/QUALITIES FEATURES FOCATION/QUALIFIES SOURCE 1. 3109 Anol_type="genomic DNA" Anoltype="genomic DNA" Anoltype="genom	######################################		301 CCCAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGAC 36

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                                  TGTTGGCGCCCTTGGCGCTTGCTGCTTGCTGCTGCAATCGGAGCAAGGTCCTCACGAGA
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/db_xref="G1:20152849"
/db_xref="G1:20152849"
/db_xref="G1:20152849"
/db_xref="G1:Q1IDDERNOLIFICATIKESCOGPHEKRLUHLLSTVNTLERPANESEPLEVKECITLQ0TIDVDERNOLITHIMLSLEWNDYNLEWNETEYGGVKDTRTPNKLWRPDVLMYNSADEGFDGTYHTNIVVKHSGSCLYVPPGIFKSTCKMDITW
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PWIKSVFLQWLPWIILMGREGKRITHKTILLENRKRELEKRSSKSLLANVLDIDD
PFHITSGSQPAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADD
EAELIGDWKFAAMVUDRFCLIVFTLFTIIATVTVLLSAFHIIVQ*
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CCPEPYVDITFT1Q1RRRTLYYFFNL1VPCVL1SSMALLGFTLPPDSGEKLTLGVT1L
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                                                                                                                                                                                      Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type III (nAcRalpha-30D) mRNA, complete cds, abra2147
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in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                         Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford
                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2033)
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Pred. No. 1.1e-193;
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/note="results in asparagine
compared to the sequence depo
Number AE003626"
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Drosophila melanogaster
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to the sequence deposited
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/organism="Drosophila
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/chromosome="2"
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379. .1863
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/gene="nAcRalpha-30D"
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/dev_stage="embryo"
1. .2023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
                                                                                            AF321447.1 GI:20152848
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LSITVFLNIVAETLEQVSDAIPLLGTYFNCIMFWASSVVLITVVLUXHHRTADIHEM
PPHIRSVFLQMLPWILLMGREGRKITRYTILLSNRWRELELKERSSKSLLANVLDIDD
DFRHTISGSQTALGSASFGRPTTVEEHHTALGCNRKDLHLILKELQFITARWRKADD
EAELIGDWRFAAMVVDRFCLIVFTLFTIATVTVLLSAPHIIVQ"
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ERPVANESEPLEVKFGLTLQQIIDVDEKNQILFTNAMLNLEWNDYNLRWNETEYGGVK
DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHNGSCLYVPPGIFKSTCKIDITW
/product="nicotinic acetylcholine receptor Dalpha6 subunit
                                                                                                                                  FPFDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEWYLLAMPGKKNTIVYA
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                                                                                                                                                                                                                                                                                      /note="results in asparagine to glycine substitution; compared to variant clone" /replace="gg"
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compared to variant clone"
/replace="9"
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/rote="compared to variant clone"
/replace="a"
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/replace="t"
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Pred. No. 1.4e-188;
O; Mismatches 405;
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/replace="t"
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                                   /protein_id="AAM13392.1"
/db_xref="G1:20152845"
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llarity 70.1%;
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-1 Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                       1490 AGGAGCTGGAGCTAAAAGGAGCGCTCCTCCAAATCCCTGCTGGCCAATGTCCTCGACATGT 1549
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//gene="nAckalpha-30D"
//note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a and
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     GGGAGCTGGAACTGAAGGAGGTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTG
                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2023)
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/organism="Drosophila melanogaster"
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Drosophila melanogaster
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                                                                                                                  1550 ACGACGACTTCCGGCACAATATCTG-
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/db_xref="taxon:7227"
/chromosome="2"
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Grauso, M. and Sattelle, D.B.
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	2023 bg melanogaster nicotin iant type II (nAcRal sly spliced. GI:20152846	Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. [(bases 1 to 2023) Grauso,M., Renan,R.A., Culetto,E. and Sattelle,D.B. Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on	KNA Mediaced A-Co-1 Fre-mana Editing Genetics 160 (4), 1519-1533 (2002) 21969411 11973307 2 (bases 1 to 2023) 2 (bases 1 to 2023) 2 (bases Submission Editional Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional	Genetics Unit, University of Oxford, South Park Road, Oxford OXI 3QX, UK Location/Qualiflers 1. 2023. /organism="Drosophila melanogaster" //mol_type="minNa" //db_xref="taxon:7227" /chromosome="2"	/map="30D1" /dev_stage="embryo" 12023 /gene="nAcRalpha-30D" /gene="nAcRalpha-30D" /note="inAcRalpha-30D"	/codoct="nicotinic acetylcholine receptor Dalpha6 subunit /product="nicotinic acetylcholine receptor Dalpha6 subunit variant type II" /protein_id="AAM13393.1" /db_xref="G1:20152847" /db_xref="G1:20152847" /translation="MOSPEPASISLEVLIFICATIKESCOGPHEKRLINHILSTYNTL ERPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLWLSLEWNDYNLRWNETEYGGVK DLRIPWERGGSCLYVPOGTEKGTCMDITW ENDANGLIGGSCLYVPOGTEKGTCMDITW ENDANGLIGGSCLYVPOGTEKGTCMDITW	FFEDDUCEMENT OF THE DENDLING WEBSTOOTH IN YAR COPERY VITTE TO THE TRANSMALL OF THE AND	/gene="nAckalpha-30D" /note="results in glycine to asparagine substitution; /note="results in glycine to asparagine substitution; compared to the sequence deposited in GenBank Accession Number AE003626" /replace="aa" /gene="nAckalpha-30D"
Db 1748 Qy 1451 Db 1808	RESULT 6 AF321446 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM. REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE	. gene CDS CDS (0)	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	77 10 variation .	17 10 7 variation
311 TGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACC 370	431 AGAGCACATGCAAGAATGGACATCGCGTGGTTTCCCTTCGACGACCCACACTGTGATATGA 490 [731 TCTCATCGATGGCACTCCTCGGCTTCACACTGCCACCAGACTCCGGAGAGAAACTCACCC 790	851 CACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGG 910 1	971 TACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCATGGATACTGC 1030	1091 GGGAGCTGGAACTGAAGGAGGTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTG 1150	GACCTGGGTGCTCAATATTCCGCACGGATTTCCGTCGGTCG	1628 TGGAGGAGCATCACGCCTGCAAACATCACAAAGATCTTCATCTTAATTCTCAAAG 1687 1331 AGCTGCAGTTCATCACGCCCAGGATGAAGAAGCTGATGAGAAGCGAGCTGATCACAGG 1390 1331 AGCTGCAGTTCATCACGCCCAGGATGAAGGCTGATGAAGCCGAGCTGATCAAGCG 1390 1688 AATTGCAATTTATTACGCCGCGATGCGCAAAGCTGACGAAGCGGAAGCGGAATTGATCGCG 1747 1391 ACTGGAAGTTTGCTGCTGCTTGTTGATAGGTTTTTCCTGTTCGTCGTTTTCA 1450
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DME554209 1665 bp mRNA linear INV 01-APR-2003 Drosophila melanogaster mRNA for nicotinic acetylcholine receptor subunit Dalpha6 (nAcRalpha-30D gene). AJ554209 AJ554209 1 GI:29466434 annormal a
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                                                                  TCTCATCGATGGCACTCCTCGGCTTCACACTGCCACAGACTCCGGAGAGAAACTCACAC
                                                                                        791 TTGGAGTCACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCCGAGACCCTGC
                                                                                                                                                                CACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGG
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1665)
Direct Submission
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670 734 730 794 790 854 850 914 910 974

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AF321448 2068 bp mRNA linear INV 29-APR-2002 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type IV (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.
                                                                                ATGATGACTTCAGACACGGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGG
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  AATTCGGTAGTTGGACTTACGATGGAAATCAGTTGGATTTGGTTTTGAGTTCCGAAGATG
                                                                                                                                                                                          TCTCATCGATGGCACTCCTCGGCTTCACACTGCCACACACTCCGGAGAGAAACTCACAC
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                                                                                                                                                                                                 /protein_id="Cad86935.1"
/db_xref="G1:29466435"
/td_xref="G1:29466435"
/tanslation="MDSPLPASLSIPVLLIFLAIIKESCOGPHEKRLINHLLSTYNTL
ERPVARESEPLEWYEGTLLQQIIDVDEKNQLLITNIMLSLEWNDYNLRWETEYGGYN
DIRTPRNKLMREPDVLMYNSADEGFOGTYHTSVVKHGGSCLIVVPFGIFKSTCKMDITW
PPFDDQHCEMRFGSWTVDGNQLDLULSESBOGGLISDFITNERWYLLERFYLLAMPGKRUTITVYA
CCPEPYVDITFFIJGTRRTLYFFNLIVPRVLISSBAGLGFTLPPDSGEKLTLGYTIL
LSLTVFLNLVAESMFTTSDAVPLIGTYFNLITWRTLLLSTRNKELEERFSKSLLAMVLDIDD
PPRHTSGSQTARTORTHERTILFRETTLILRENGERSKSLLAMVLDIDD
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Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, University College London, Gower Street, London, WCIE 6BT, UNITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTGGCGCCCTTGGCTGCTTTGCTGCCCGTATCGGAGCAAGGTCCTCACGAGA
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/product="nicotinic acetylcholine receptor
Dalpha6"
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/product="nicotinic acetylcholine receptor
Dalpha6"
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Pred. No. 9.8e-
0; Mismatches
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                                                               /organism="Drosophila
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                   /gene="nAcRalpha-30D"
122. .1525
                                                                                                                       /gene="nAcRalpha-30D"
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                                       Location/Qualifiers
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 /note="compared to the sequence deposited in GenBank
Accession Number AE003626"
                                                                                            GenBank
                                                                                                                                                                                    /note="compared to the sequence deposited in GenBank
Accession Number AE003626"
                                                                                                                                                                                                                                                                                                                                     87;
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                                                                                            /note="compared to the sequence deposited Accession Number AE003626"
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Pred. No. 4.8e-179;
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                                                                                                                                                               Grauso,M., Reenan,R.,, Culetto,E. and Sattelle,D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6, and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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VLWTHRFADIHEMPPWIKSVFLQWLPWILMAGRPGKLTFRCTILLSNRMKELELKE
VSSKSLLANVLDIDDDPRHTISGSGASTGFRTTVEEHHTATGCNHKDLHLIL
KELQFITARWRKADDEAELIGDWKFAAMVVDRPCLIVFTLFTITATVTVLLSAPHIIV
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ERPANESEBEPLEVKECTIQQIIUDDEKNQILITNAHLMIDERNQLITHYMLSEBEWN
DYNIKWHEFEYGGYGLRIPPKLMKEWREDVLAW'NSADEGEPGTYHTNITVYKEGSCLYV
PPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEW
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                                                                                                                                                                                                                                                                                              Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
30x, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="results in arginine to histidine substitution; compared to the sequence deposited in GenBank Accession Number AE003626"
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                                                                                          Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
I (bases 1 to 2069)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="lon channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3a, 8b; contains two repeats of the functional domain lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="nicotinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
Mod_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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/note="results in serine
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Number AE003626"
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/protein_id="AAM13395.1"
/db_xref="G1:20152851"
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379. .1908
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1. .2068
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                   GI:20152850
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AF321448.1
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CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
LSILYFLNIVASEMPTTSDAVPLIGYTILLSLTVFLNLVABETLPQVSDAIPLLGTYFN
CIMPWVASSVVLTVVVLNYHHRTADIHEMPPMIKSVFLQMLPWILRMGRPGRKITRKT
ILLSNRWKELELKERSSKSLLAMVLDIDDDFRHTISGSQTALGSSASFGRPTVEEHH
TAIGCNHKDLHLILKELQFITARMRKADDGAELIGDWKFAAMVUDRFCLIVFTLFTII
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                                                                                                                                                                                                                                                                                                                                                                                         /note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a, 8a an
8b; contains two repeats of the transmembrane TM2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="nAcRalpha-30D"
/note="results in methionine to isoleucine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                  11973307
2 (bases 1 to 2110)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 TGTTGGCGGCCTTGGCGCTGCTTGCTGCCGGTATCGGAGCAAGGTCCTCACGAGA
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Accession Number AE003626"
/replace="c" 516 g 494 t
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                      /gene="nAcRalpha-30D"
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1. .2110
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                                                                                                                                                                                                                                                                                                                                                                       GGAAGAAGATCACCAGGAAGACTATAATGATGAACACGAGGATGAGGGAGCTGGAACTGA 1105
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Drosophila melanogaster
Drusophila melanogaster
Drosophila melanogaster
Bukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 2110)
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Novel Putative Oroserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                     866 CTATCCCCCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGGTAGCGTCGTCGTGG 925
                                                                                                                                                                                                                                    TTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCCGAGACCCTGCCACAGGTCTCCGACG
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AF321449
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131 AGAGCGAACCGCTAGAGGTCAGGTTCGGCTTGACCTTGCAGAAATCATTGACGTGGACG 190	191 AGAAGAATCAACTACTTATAACCAATATATGCCTGTCGTTGGAGTGGAATGACTACAACC 250	TGAGGTGGAACGACGGGTATGGCGGTCAAGGACTCAGGATCACACACA	TGTGGAAGCCGGACGTCTTATGTATATATATATGTGCTGACGAGGTTTTGACGGGACCTACC	rGregaagccccacgregreargracaacacccccarreagregarregar	371 AGACCAACGIGGTCAGAAGCGCCGCAGTTGCCTGTACGTGCCACCTGGCATATTCA 430 	431 AGAGCACATGCAAGATGGCATGGGTTCCCTTCGACGACCACCTGTGATATGA 490 	491 AGTICGGIAGCIGGACAIAIGACGGCAAÏCAGTIGGAICTGGIGCIAAAAGAIGAGGGCAG 550 	551 GCGCGATCTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCA 610 	AAAAAAAAAAATAACATACGCGGCGCCCCGGGCCCTACGTCGCCCTTCACCA	1010 AGAAGAATACGATAGTCTACGCTGCTGCTGCAAACCATATGTCGATATCACCTTTACTA 1069	671 TCATGATAAGAAGACGAACCTTGTACTTCTTCAACCTGATCGTCCCGTGCGTG	731 TCTCATCGATGCACTCCTCGGCTTCACACTGCCACAGACTCCGGAGAAACTCACAC 790 	79	1190 TGGGCGTAACTATACTATCATTAACAGTATTTCTAAACCTTGTCGCCGAGTCCATGC 1249	791	824 TCCTCAACCTGGTAGCCGAGACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTTAGGGA 883	884 CGTACTTCAATTGCATCATGTTCATGGTAGCGCGTCTGTGGTACTGTGGTGCTGC 943 	TCAATTACÇACCATCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTAT 100		1064 AGACTATAATGATGAGGGGTGAGGAGCTGGAAGTGGAGGAGAGGTGGTCGAGT 1123 	
. yo da	oy 4	8 % E	2 6	qa ;	oy O	Qy Db	Qy Db	, YO E	δγ	qa	oy Op	λ Q	δγ	QQ	Qy Db	oy Db	oy da	oy og	ç, dg	Qy	

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Bukaryotts; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glosata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.

Schulte, T., Oellers, N. and Adamczewski, M.
Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Ce21
than to other insect nicotinic acetylcholine receptor alpha
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Heliothis virescens putative nicotinic acetylcholine receptor alpha 7-1 subunit mRNA, complete cds.
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YNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDF
GGVKDLRVPPRHLMKPDVLMYNSADEGEDSTYFTNVVVRNNGSCLYYPPGIFKSTKI
DITWFPFDDQRCEMKFDVLMYYDGYQLDLQLQDEGGGDISFYTNGEWELIGVPGKRNE
IYYNCCPEPYIDITRAFUYRRYLLYYPFNLIYPCVLLASMALLGFTLPPDSGEKLSLG
VTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFWVASSVVSTILILNYHRRAD
THEMSDWIRCVFLYWLPWVLRNSRPGSATTPPPARVPPPDLELRENSSKSLLANVLD
1124 CCTTGCTGGCGAATGTTCTAGATATTGATGATGACTTCAGACACGGCCCTCCGCCTCCTA 1183
                                                                                                                     1184 ACAGTACTGCCTCGACCGGGAATTTGGGACCTGGGTGCTCAATATTCCGCACGGATTTCC 1243
                                                                                                                                                                                -----GCTCCCAAACCGCCATTGGCTCGT 1687
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Schulter, T. Oellers, N. and Adamczewski, M.
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG, Bldg. Q 18,, Leverkusen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1364 CTGATGAGGAAGCCGAGCTGATCAGCGACTGGAAGTTTGCTGCATGGTTGATAGGT
                                     1. 3629

^Organism="Heliothis virescens"

/mol_type="mRNA"

/db_xref="taxon:7102"
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/db_xref="G1:4895005"
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/note="hvnachra7-1"
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 ATACTGCGAATGTCGAGGCCAGGGAAGAACACCAGGAAGACTATAATGATGAAGACACG -1083
                                                                                                                                                                                                                                     ATCAGCGACTGGAAGTTTGCTGCATGGTTGTTGATAGGTTTTGCCTGTTCGTGTTCACA 1443
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                                                        1084 AGGATGAGGGAGCTGGAACTGAAGGAGAGGTCGTCGAAGTCCTTGCTGGCGAATGTTCTA
                                                                                                                                                                 Adamczewski,M.D., Schulte,T.D. and Oellers,N.D.
Wouleler acids encoding acetylcholin-receptor subunits from
Patent: EP 0962528-A 3 08-DEC-1999;
BAYER AG (DE)
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953 c 944 g 910 t
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Heliothis virescens
Heliothyda; Metazoa, Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Lepidoptera; Glossata; Dit
Noctucidea; Noctuidae; Heliothinee; Heliothis.
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/note="unnamed protein product"
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931 c 922 g 895 t 1 others
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Pred. No. 1.1e-141;
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PAT 06-SEP-2000

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 1448 CCGCCGCCGGACCTGGAGCTGCGCGAGCGCTCCTAGCGTGCTCCTAGCGAACGTGCTC
                               GATATTGATGATGACTTCAGACACGGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGG
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JP 2000023680-A/2.
Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Lepidoptera; Glossata; Dirrysia;
Noctuoidae; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3701)
Martin,A., Nadja,E. and Thomas,S.
Mucleic acid encoding insect actyl choline receptor subunit
Patent: JP 2000023680-A 2 25-JAN-2000;
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PR 04-MAY-1998 DE 19819829.9
PI MARTIN ADAMUTSUEUSUKI, NADJA ERASU, THOMAS SCHULTE PC
C12N15/09, A01K67/033, C07K14/7705, C07K16/28, C12N1/21, C12N5/10,
C12Q1/68,
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0; Mismatches 460; Indels
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/mol_type="genomic DNA"
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/ Lranslation="WSFPQPHSLPEATANGGRMLVYGLGLLIMIPACAAGPHEKRLLH
ALLDNYNSLERPVVNESDEPLÖLSFGLTLMQ1IDVDEKNGLLTYNIWIKLEWNDMNLRW
NSSEFGGVRDLRIPPHRLWKPDVLMYNSADEGFDGTYATNVVVRNNGSCLYVPPGIFK
STCKIDITWRPFRDDQRCEMRFGSWTYDGFGLDLQLOBAGGDISSFITNGEWDLLGVP
GRRNEIYYNCCPEPYIDITRRFTLXYFFNLIYPGVLIASWALLGFTLPDSGE
KLSGATILLSLTVFLNMVAETMPATSDAVPLLGKYFNCINFWYASSVYSTILVLNYH
HRRPDTHEWSEWIRYIFLYWLPCINRWQRPQQYGYECPPPESSSSSASGEKKQOION
VELKERSKSKLLAMVLDIDDDFRCNHRCASATLPHQPTYYRTWYRQGDGGSVGPA
GPWVDGRLHBAISHTCLTSSAYFELALILKELRWITEOLKKEDETSDITRDWKFAAMV
VDRLCLIIFTLFTIIATLAVLFSAPHFIVSGVRG"
                                                                                                   INV 01-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S., Department of Pharmacology,
Street, London, WClE 6BT, UNITED
                                                                                                                                                                                                 CITITICACAATCATCGCGACAGTAGCTGTCCTGTTATCGGCACCGCATATCATCGTG 1500
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                             TCCACGATGGAAGACGTGGGCGGCGGGCTGGGTAGCCACCATCGCGAGCTGCACCTCATA
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Submitted (31-MAR-2003) Millar N.
University College London, Gower
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    1683
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Db	Qy 1303	RESULT 14 AF272778 LOCUS LOCUS DEFINITION Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5 BEFINITION BUDILIT (NACRalpha-34E) mRNA, NACRalpha-34E-A allele, complete cds. ACCESSION AF272778 AF272778 AF272778 AF272778 AF272778 COURCE CORGANISM Drosophila melanogaster (fruit fly) Neoptera; Endopteraygota; Drosophila melanogaster BURATYOTA: BEFERENCE AUTHORS TITLE AUTHORS Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a Nova Mediated A-for T pre-mRNA Feling on REFERENCE AUTHORS AUTHORS Nova and Highly Conserved Target of Adenosine Deaminase Acting on RANA Mediated A-for T pre-mRNA Felithna	JOURNAL Genetics 160 (4), 1519-1533 (2002) WEDLINE 2195411 PUBRED 1973307 REFERENCE 2 (bases 1 to 2907) REFERENCE Grauso, M. and Sattelle, D.B. AUTHORS Grauso, M. and Sattelle, D.B. TITLE Direct Submission JOURNAL Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, JOURNAL University of Oxford, South Park Road, Oxford Oxl 3Qx, UK FEATURES Location/Qualifiers Location/Qualifiers Source 12907 /db_rref="taxon:7227" //map="12.; 34E4-5" //map="12.; 34E4-5" //de_stage="embryo" /gene="nackalpha-34E"
Best Local Similarity 61.0%; Pred. No. 4.5e-131; Matches 942; Conservative 0; Mismatches 540; Indels 63; Gaps 19 GCCTTGGCGTGTGGCTTTGCTGCCCGTATCGGACAGGTCCTCACGAGAAGAGCTC	Db 272 CAACTGCTTATAACGAATATTTGGCTCAAATTGGAATGGAACGATATGAATCTTCGATGG 331 Oy 259 AACGACGCGAGTATGGCGGGTCAAGGACCACACACACACA	Qy 499 AGCTGGACATATGACGATCAGTTGGTGCTAAAAGATGAGGCGGCGAT 558 1111 11 11 11 11 11 11 1	799 ACTATCTTCTATCGCTGACGTGTTCCTCGACGCGGGGCCCTGCCACGTG 799 ACTATCTTCTATCGCTGACGTGTTCCTCGACGTGGCGGGGCCCTGCCACGTG 1 1 1 1 1 1 1 1 1 1

7899. 2712 70040.2102. 2012 70040.2102 70	177 CATTGACGGGAGGAAAAACAACCATTATAACCAATATAAGGCTGTCGAGGGG	GCCTGTTCGGACTGCCCAGGACGACGACGACGACTGATCCCGACCAC 223
7899 2712 7990 7212 7990 700. channel, neurotransmitter transmembrane 700.ce=100 channel, neurotransmitter transmembrane 700.ce=100 channel, neurotransmitter transmembrane 700.00.512.1.		
Lion	// Mote="nacRalpha-34g" // Mote="nacRalpha-34g" // Mote="nacRalpha-34g" // Mote="nacrannel; neurotransmitter transmembrane receptor" // Codon_start=1 // Product="nicotinic acetylcholine receptor balpa5 subunit="nicotinic acetylcholine receptor balpa5 subunit="nicotinic acetylcholine receptor balpa5 // Protein_id="AshWAGMKITEDDDEMIAVRAHCSSWFSSRSTRTMSSNGRH // Moter_10="nicotinic acetylcholine receptor balpa5 // Moter_10="nicotinic acetylcholine receptor balpa5 // Protein_id="AshWAGMKITEDDDEMIAVRAHCSSWFSSRSTRTMSNRSHWENDWITEDDEMIAVRANDENDWITEDDEMIAVRANDENDWITEDRINGSRSSSSSSSSSSSWFTSSWRSTRTMSTRYTMST	/replace="g" 42 g 634 t 535 a 696 c 642 g 634 t 536 c 652 c

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/translation="MRNAQLKLTEVDDDELWLAVRLAHCSSNISSSSTRTTSSNQRH
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nmlspktaaaataagdeattqoptnirlcarkrorlrrrrrrrrpatpnetdirkoqol
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
AGACGTGGGCGGGCTGGGTAGCCA------CCATCGCGAGCTGCACCTCATACT
                                                                                                                                                                                   CAGCGACTGGAAGTTTGCTGCGATGGTTGTTGATAGGTTTTGCCTGTTCGTGTTCACACT
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                                                                                                                                     2532 AAAGGAAATTCGCTTTATAACTGATCAGCTACGTACGTAAAGATGACGAGTGCAATGACATTGC
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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1 3QX, UK
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Submitted (26-MAY-2001) MRC-FGU Human Anatomy and Geneti
University of Oxford, South Parks Road, Oxford OX1 3QX,
Location/Qualifiers
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/organism="Drosophila
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SMPPFKTRKSTDTYSTPAAITSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLH
VLQVLLVSLQQWQLHVQQRSVLLFRRIAASTIAFISYLGSFAAQLRSSSSSSNSNS
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SDPLQLSFGLTLAQIIDVDERNQLLYNWWIKLEWNDMNLRWNTSDYGGVKDLRIPPH
RIWKPDVLMYNSABEFBGTYQTNVVYRNNGSCLYVPPGIFKSTCKIDITWFPFDDQR
CEMKFGSWTYDGFQVCPANVTRSITTAARNPI"
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1016 2098 .	1065 2158		2218	1166	2278	1215	2338	1274	2398	1325	2458	1385	2518	1445	2578			
7 TCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTT	7 GCCATGGATACTGCGAATGTCGAGGCCAGGGAAGAAGATCACCAGGAAG	ACTATAATGATGAAGAGGATGAGGAGGAGCTGGAACTGAA		GAGAGGTCGTCGAAGTCCTTGCTGCCGAATGTTCTAGATATTGATGATGATCACACACA	2219 AGAĞCĞCTCĞTCĞAAATCĞCTĞCTĞĞCCAACĞTACTAĞACATCĞATĞATĞATĞATÇTCÇĞCA	1167 CGGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGGGACCT	CAATTGTCGCCCCATGACGCCCGGCGGAACACTGCCACAAACACCCGGCTTTCTATCGCAC	GGGTGCTCAATATTCCG-CACGGATTCCGTCGGTCGTTCGTCCGTCCGTCCGTCCACGATGGA	GGTTTATGGACAAGGCGACGATGGCAGCTTGGCCAATTGGCAGCACCCGAATGCCGGA	AGACGTGGGCGGGGGGTGGGTAGCCACCATCGCGAGCTGCACCTCATACT	2399 TGGGTCACCCATCATACGTGCATCAATCATCAACTGAATATGGATTAGGTTTAATCTT	S GAGAGACTGCAGTTCATCACGCCAGGATGAAGAAGGCTGATGAGGAAGCCGAGCTGAT	2459 AAAGGAAATTCGCTTTATAACTGATCAGCTACGTAAAGATGACGAGTGCAATGACATTGC	CAGCGACTGGAAGTTTGCTGCGATGGTTGTTGATAGGTTTTGCCTGTTCGTGTTCACACT	CAATGATTGGAAATTTGCAGCTATGGTCGTTGACAGACTGTGCCTTATCATATTCACAAT		GTTCGCAATATTAGCCACAATAGCTGTACTACTATCAGCACCACATATTATTGT 2632	
957	1017	1066	2159	1107	2219	1167	2279	1216	2339	1275	2399	1326	2459	1386	2519	1446	2579	
oy Dp	Oy Dp	Qy	QQ	٥y	QQ	ογ	g G	δγ	g	δy	ф	Οy	· Dp	Οy	q	Qy	qa	

Search completed: August 21, 2003, 09:54:23 Job time : 5608.3 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 13, 2003, 15:21:20 ; Search time 47.4386 Seconds (without alignments) 2698.100 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-303-232-4 2665 1 MGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHINVS 496

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:* sp_vertebrate:*
sp_unclassified:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:* sp_plant:*
sp_rodent:*
sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

				heliothis v	ophila	ophila	othis v	ophila	musculu	lus gall	orhabdi	orhabdi							
			Description	Q9xzi3 helic	Q8t7v5 drosc	Q9vwi9 drosophila	Q9xzi4 helic	Q8t7s2 drosc	Q8t7s1 drosc	Q8t7s3 drosc	Q8t7s0 drosc	Q8t7r9 drosc	Q9v179 drosc	Q8ipe2 drosc	Q9vjt9 drosc	Ogjhd6 mus	Q03481 gal]	P91197 caend	Q8i932 caenorhabdi
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			Score	2665	2064.5	2046.5	1803.5	1795.5	1792.5	1790.5	1774	1769	1484.5	1371	1279	1242	1219.5	1141	1113
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Ognkdl drosophila 062083 caenorhabdi 018556 caenorhabdi 046128 heliothis v 040941 myzus persi	046133 locusta mig QBmur0 apis mellif QBtOy9 aplysia cal QBmm21 aphis gossy Q9vc74 drosophila	Ognfx8 myzus persi Ognfr8 myzus persi P91765 myzus persi Og1x60 mus musculu	096631 heliothis v Q@Whh6 mus musculu O46134 locusta mig O8r499 mus musculu Q@Br44 mus musculu	
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ALIGNMENTS

RESULT 1 09X213	Q9XZI3 PRELIMINARY; PRT; 496 AA. Q9XZI3;		01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		heliotnis virescens (Noctulu Moth) (Owiet Moth). Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		Noctuidae; Heliothinae; Heliothis.		SEQUENCE FROM N.A.			more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than										FIGURE FOLDSON, NEGLEGIBLES, 1. PRINTS: PRO0252: NRIONCHANNEL.			_	Transmembrane.	SEQUENCE 496 AA; 56347 MW; 8032FED8515A6210 CRC64;	Onery Match 100.0%: Score 2665: DB 5: Length 496:	Cimilarity 100 08. Dred No 1 36-244.
RE.	A D	DT TQ	ď	DE	38	8	88	Z.	RP	RA	RŢ	RT	RŢ	RL	ပ္ပ	ပ္ပ	DR	DR.	DR.	ž 5	5 2	2 2	DR.	DR	ΚX	ΧX	SO	_	

ö Gaps ö Indels Best Local Similarity 100.0%; Pred. No. 1.3e-244; Matches 496; Conservative 0; Mismatches 0; a

6;

Gaps

136 414 196

474

256 534 316 374 651

354

92

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Admis M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admas M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutron G.G., Wortman J.R., Yandell M.D., Chanpe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Chanpe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendelle J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                         SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVA
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                    Length
                                                                                                              Indels
                     C8B4F6B34287C8C8 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                 DB 5;
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  MGGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
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-- SUBCELLUAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

EMBL; AF272778; AAM13390.1; --
FIYBASE: FEGROUSSES: AAR-ALLEAR RESEARCH FAMILY.

FIYBASE: FEGROUSSES: AAR-ALLEAR RESEARCH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha5 subunit.
NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR CG4498 OR CG16878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)..
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR006202; Neur_chan_LBD.
Ffam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_memb; 1.
TIGRAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
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61517 MW; 7B83025107A66209 CRC64;

545 AA;

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                                                                                     39 GPHEKRLLHALLDNYNSLERPVVNESDPLØLSFGLTLAQIIDVDEKNQLLITNIWLKLEW
                                                                     31 GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW
                                                                                                                                                                                                              PGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELI
                                                                                                                                                                                                                                GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                                                                                219 GVPGKRNEIYYNCCPEPYIDITFAILIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 DLELRERSSKSLLANVLDIDDDFR--HPQA-----QQPQCCR-YYRGGEENGAG----
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative nicotinic acetylcholine receptor alpha 7-2 subunit.
Heliothis virescens (Noctuid moth) (Owlet moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Leptdoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Schulte T., Oellers N., Adamczewski M.;
Schulte T., Oellers N., Adamczewski M.;
"Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AF143847; AAD32698.1;
                                    45;
   545;
   Length
                                    Indels
   DB 5;
                                    36;
 76.8%; Score 2046.5; DB 5 77.7%; Pred. No. 9.4e-186;
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                                  32; Mismatches
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Interpro; IPR006202; Neur_chan_LBD.
Interpro; IPR006029; Neu_channel_memb
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Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                    Conservative
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Query Match
Best Local Similarity
Matches 394; Conserv
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                                                                                                                       DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                                                                                       12 APAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII
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                                                                                                                                                                                                                                                                                                                                                                                                       PPPPDLELRERSSKSLLANVLDIDDDFRH----PQAQQ-----PQCCRY---YRGG---
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21969411; PubMed-11973307; Grauso M.; Reenan R.A., Culetto E., Sattelle D.B.; Grauso M.; Reenan R.A., Culetto E., Sattelle D.B.; Movel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-T Pre-mRNA Editing."; Genetics 160:1519-1533(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AF321446; AAM13393.1; -.
Flybase; FB9n0032151; nAcR-alpha-30D.
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                          Score 1803.5; DB 5; Length Pred. No. 1.1e-162;
                                                                                   Indels
                                   56704 MW; 43CB0DC3960C78AB CRC64;
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1. Glycoprotein; Ionic channel; Postsynaptic membrane;
                                                                                   78;
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                                                          67.7%; Score 1803.5; 68.7%; Pred. No. 1.16
                                                                                   Mismatches
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                                                                                   53;
                                                                      Best Local Similarity 68.79
Matches 347; Conservative
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                                    501 AA;
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SEQUENCE FROM N.A.
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                         Transmembrane
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                                   SEQUENCE
                                                           Query Match
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MEDLINE=21969411; PubMed=11973307;
MEDLINE=21969411; PubMed=11973307;
MEDLINE=21969411; PubMed=11973307;
MEDLINE=21969411; PubMed=11973307;
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                     494;
                                                                                                        PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1. Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                          Indels
                                                                                                                                                              6EE711810EDE7BBB CRC64;
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23, Last annotation update)
                                                                                                                                                                                                 ; Score 1795.5; DB 5;
; Pred. No. 6.1e-162;
54; Mismatches 81;
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                                                                                   TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
               Neur_chan_LBD.
Neu_channel_memb
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                             InterPro; IPR006629; Neu channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                56048 MW;
                                                                                                                                                                                                     67.48;
68.18;
                                                                                                                                                                                                                                      342; Conservative
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IPR006201;
IPR006202;
                                                                                                                                                                494 AA;
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SEQUENCE 49
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Transmembrane
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                                                                                                                                                                                                                                                                                                          LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADDEAELIGDWKFAAMVVDRFCLI 471
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                                                                                                                                                                                                                                                          SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing.";
Genetics 160:1519-1533(2002).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY:
EMBL; AF321447; AAM13394.1; -
FlyBase; FBgn0032151; nAcR-alpha-30D.
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last aenotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type INACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                               494;
                                                                                                                                                     PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                     81; Indels
                                                                                                                                                                                        494 AA; 56113 MW; 48327537229573FF CRC64;
                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                             tch 67.3%; Score 1792.5; DB 5 al Similarity 67.9%; Pred. No. 1.2e-161; 341; Conservative 55; Mismatches 81;
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                                                                                InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
IGRFAMS; TIGR00860; LIC; 1.
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                                                                                                                                                                             Transmembrane
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                                                                                                                                                                                       SEQUENCE
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type IV.
                                                                                                                                                                                   IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
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Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                         -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 AA; 56095 MW; B46EBEDA63A92942 CRC64;
MEDLINE-21969411; PubMed-11973307;
Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
"Novel Putative Nicotinic Acetylcholine Receptor S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.2%; Score 1790.5; DB 5
67.9%; Pred. No. 1.8e-161;
live 53; Mismatches 83;
                                                                                                                                                                                                                                                                       InterPro; IPR006202; Neur_chan_LBD.
InterPro; IRR006029; Neur_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                        FlyBase; FBgn0032151; nAcR-alpha-30D.
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                                                                                                                                                                                                                                                    InterPro; IPR006201; Neur_channel
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Matches 341; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                 -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AF321448; AAM13395.1; -.
                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                         Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128
           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                             509 AA; 57887 MW; BE8D8E0198E0C2BD CRC64;
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Pred. No. 7.1e-160;
4; Mismatches 82;
                                                                                                                                                                                                                                             Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGREAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                  FlyBase; FBgn0032151; nAcR-alpha-30D. InterPro; IPR006201; Neur_channel. InterPro; IPR006202; Neur_channel_memb. InterPro; IPR006029; Neu_channel_memb.
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                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                            SEQUENCE FROM N.A.
                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                      Transmembrane
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Best Local Simi
Matches 341;
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- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- PLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP-PPPDLELRERSSKSLLANVLDIDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRHPQAQQPQCCRYYRGGEENGAGLAA------HSCFGVDY-ELSLILKEIRVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMV 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                      01-JUN-2002 (TrEMBLE). 21, Last sequence update)
01-MR-2003 (TrEMBLE). 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     523 AA; 59110 MW; 1C200AF74F87F841 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1769; DB 5;
Pred. No. 2.2e-159;
  Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGRRAMs; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0032151; nAcR-alpha-30D
                                                 Created)
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 64.4
Matches 342; Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRHTIS-
                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane
                                                 01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423
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445

RESULT Q8T7R9

us-09-303-232-4.rspt

RC STRAIN—BERKELEY:

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams M.D., Celniker S.E., Richards S., Ashbuner M., Hedelsen S.N., R. Getton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Batton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Bratch G.C., Batton G.G., Mank K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., A. Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S., Bortway D., Botchen M.R., Bouck J., Brotstein D., Bolshakov S., Bortway D., Suller R., Doyle C., Davengor L.B., Davies P., Borther A., Danle C., Davengor L.B., Davies P., Botcher A., Danle C., Davengor L.B., Davies P., Botcher A., Davies M., Doyler C., Gabrieliar A.C., Garg N.S., Gelbart W.M., Glasser K., Burtis N.L., Baver B., Burtis N.L., Baver B., Beland B.C., Gargilster G.C., Ferraz C., Ferriard S., Pleischman W., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jasko P., Lel Y., Laveryo D., Helman T.J., Herandez S., Rulp D., Lai Z., Lang Y., Matton D., Houston K.A., Moyl M., Wolland T.J., Wall M.-H., Thegwam C. M., Matton B., Molland T.C., Morris J., Machin D., Matton D.L., Marko P., Lel J., Li Z., Liang Y., Lin X., Lasko P., Lel J., Lavier C., Morris J., Machin G., Steneller F., Shen H., Andres B., McIntosh T.C., Morris J., Muzph W., Moyler J., Marko M., Strong R., Shen B., Shen S., Pollard J., Sheng L., Sheng R., Wallskas R., Tector C., Turner R., Venter E., Wall Schone, S., Shen R., Helmor S.H., Wells R., Worley S., M Celniker S. E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galler R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacieb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., CG4128 protein.
NACR-ALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Created)
Last sequence update)
Last annotation update) 554 Ephydroidea; Drosophilidae; Drosophila. PRT; 13, 22, 01-MAR-2003 (TrEMBLrel. 23, Science 287:2185-2195(2000) PRELIMINARY; (TrEMBLrel. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI_TaxID=7227; 01-MAY-2000 01-OCT-2002 RESULT 10 **09VL79** g

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-----ILFFQFN----CAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | :| |: |: |: |: |: |----GSOTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADDEAELI 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLQLQDEGGGDISSFVTNGEWELIGV-PGK------RNEIYYNCCPEPYIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 CRRVHADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQCRAERVTILLSLTVELNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWVLRMSRPGSATTPPPARVP-PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYRGGEENGAGLAA------HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMQIIDVDEKNQLLITUIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALLGFTLPPDSGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --VTILLSLTVFLNMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 117; Gaps
                                                                                                       Misra S., Croshy M.A., Matthews B.B., Bayraktaroglu L., Campbell I Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N. Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Saarle S.W.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                       FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003626; AAF52817.2; -.
                                                                                                                                                                                                                                                         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRPAMS; TIGR00860; LIC; 1.
PROSITE; P00236; NEUROTR_ION_CHANNEL; 1.
SEQUENCE 554 AA; 63236 MW; D6C63EB7F5B32A35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.7%; Score 1484.5; DB 5 Best Local Similarity 53.6%; Pred. No. 2.7e-132; Matches 310; Conservative 53; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KLSLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006201; Neur_channel.
InterPro; IPR006029; Neu_channel_memb.
                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0032151; nAcR-alpha-30D.
                                                                                        SEQUENCE FROM N.A. Misra S., Crosby M.A., Miradecky P., Huang Y., K. Tupy J.L., Bergman C., Br. Clamp M., Drysdale R., El
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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350 406 409 459 457 œ

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RESULT 12
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RADAGRAMS NA.
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
ADAGRAMS M.D., Celniker S.E., Holt R.A., Edans R.A., Galle R.F.,
RADAGRAMS C., Rotraman J.R., Yanafoll M.D., Zhang Q., Chen.L.X.,
RADAGRAMS C., Rotraman J.R., Yanafoll M.D., Zhang Q., Chen.L.X.,
RADAGRAMS C., Rotraman J.R., Yanafoll M.D., Edang Q., Chen.L.X.,
RADAGRAMS M., Bazel R.G., Champe M., Pfelifer B.D.,
RADALI J.F., Agbayani A., Bazel R.G., Champe M., Pfelifer B.D.,
RADALI J.F., Agbayani A., Bazel R.G., Champe M., Pfelifer B.D.,
RADALI J.F., Doyle C., Balch H.J., Bouck J., Borckstein P., Borchisakov S.,
Borkova D., Botchan M.R., Bulck H., Cadieu E., Center A., Chandra I.,
RADAGRON R., Doug L.E., Downes M. Dugan-Kocha S., Ploukov B.C., Dunn P.,
RADAGRON R., Doug L.E., Downes M., Dugan-Kocha S., Platschmann W.,
RADAGRON R., Doug L.E., Downes M., Dugan-Kocha S., Platkov B.C., Dunn P.,
RADAGRON R., Doug L.E., Downes M., Dugan-Kocha S., Platschmann W.,
RADAGRON R., Doug L.E., Downes M., Dugan-Kocha S., Platschmann W.,
RADAGRON R., Doug L.E., Downes M., Dugan-Kocha S., Platschmann W.,
RADAGRON R., Doug L.E., Mays A.D., Dow I., Diez S.M.,
AUSTIN D., Houston R.A., Howlann T.J., Hernandez J.R., Rotter B., McIntosh T.G., Ranali M., Kalush F., Karpen G.H., Wei M.H., Ibeywam C.,
RADALI M., Malush F., Karpen G.H., Marzhy D.M., Nelson D.L.
RADAGROP D., Revitsky A.A., Li J., Li Z., Ling Y., Lin X.,
Alali M., Malush B., McIntosh T.C., Morris J. Morrhy B., Murphy L., Muzny D.M., Nelson D.L.
RADAGROP D.R., Nalaman G.S., Pan S., Pollard J., Wellow R., Shen H.,
Radacalo M., Pittaman G.S., Pan S., Pollard J., Wenger B.,
Radacalo M., Pittaman G.S., Pan S., Pollard J., Wenger B., Smith T.,
Radagor R., John M., Nator R., Nixon K., Nusskern D.R., Pacleb J.M.,
Radios R., Wessarman D.A., Weinstock G., Zhon K., Waller B., Wolley R.W., Woodagor, Wolley R.W., Wolley M., Wolley R.W., Strong C., Pan R.,
Radios S., Werker B.W., Rubin G.W., Strong R., Shin H. P.,

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Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Barson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferritera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
RDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMV 495
                  516 GDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIV. 553
                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                            525 AA
                                                                                                                                                                Created)
                                                                                                                            PRT;
                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:2185-2195(2000).
                                                                                                                            PRELIMINARY;
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458
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Q8IPE2
Q8IPE2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 CRRVHADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQCRAES-----TYFNCIM 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALLGFTLPPDSGEKLSLGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 -----ATSDAVPLLGTTVFLNMVAETMP-----ATSDAVPLLGTYFNCIM
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                                                                                                                                                             Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bernman E., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M., J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Annotation of Drosophila melanogaster genome.";
  Tector C., Tyler D.,
, Venter J.C., Rubin G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.4%; Score 1371; DB 5; Length 525; Best Local Similarity 52.2%; Pred. No. 1.6e-121; Matches 290; Conservative 56; Mismatches 108; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003626; AAN10709.1; -
SEQUENCE 525 AA; 60135, MW; CF95283C56EA90A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                   to the EMBL/GenBank/DDBJ databases
Stapleton M., Strong R., Svirskas R., Tector C. Williams S.M., Zaveri J.S., Smith H.O., Venter "Sequencing of Drosophila melanogaster genome."
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                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Amanatides G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
Amanatides G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
Scherer S.E., Richards S.C., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X.,
Bradon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow R.M., Basu A., Baxendala J., Baytaktarolu L., Beasley E.M.,
Besson K.Y., Benco P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burkova D., Botchan M.R., Boulk J., Brokstein P., Brother P.,
Burkova D., Botchan M.R., Boulk J., Brokstein P., Brother P.,
Burkova D., Buller H., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart M.M., Glasser K.,
Glodek A., Gong F. Gorrell J.H., Wei M.-H., Ibeyam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lia Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lia X.,
Liu X., Mattel B., Morfluch T.C., Morris J., Woshrefi A.,
Merkulov G., Milshina N.V., Wobarry C., Morris J., Woshrefi A.,
Relazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Wassen D.L.,
Rander K., Remington K., Saunders R., Vencheler F., Wang X.,
Wang Z.-Y., Wassamman D.A., Walnstene E., Wang A., Wang X.,
Wang Z.-Y., Wassamman D.A., Walnstene E., Wang G., Zhao O., Zhang C.,
Steiner K., Wayer S., Wholey M., Zhou X., Zhu S., Zhao O., Zhao O
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A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

A Ferfiera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
CG4498 protein.
NACR ALPHA - 34E OR NACRALPHA - 34E OR BG:DS05899.4 OR BG:DS05899.5 or CG4498 OR CG16878.
                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
273 AA.
                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
 PRELIMINARY;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQV- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 LIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTY 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 LQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFN
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        Campbell K.,
th C.D.,
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Purpy J.L., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Bermant D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
SEQUENCE 273 AA; 31655 MW; CA95F19953E37248 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
48.0%; Score 1279; DB 5;
Best Local Similarity 57.6%; Pred. No. 3.7e-113;
Matches 247; Conservative 19; Mismatches 7;
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Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0028875; nAcR-alpha-34E
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InterPro; IPR006202; Neur_chan_LBD.
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HSSP; P58154; 119B.
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ENGAGLAAHSCFGV------DYELSLILKEIRVITDQMRKDDEDADISR 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDKVRPACQHKP------RRCSLASV-ELSAGAGPPSSNGNLLYIGFRGLEGMHCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                     Stitzel J.A., Farnham D.A., Collins A.C.;
"Linkage of strain-specific nicotinic receptor alpha 7 subunit
restriction fragment length polymorphisms with levels of alpha-
bungarotoxin binding in brain.":
                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00252; NRIONCHANNEL.
TIGRERMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NBUROTE ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         502 AA; 56617 MW; C9353E5136D620E3 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Nicotinic acetylcholine receptor subunit alpha.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.6%; Score 1242; DB 11;
47.1%; Pred. No. 2.7e-109;
ative 90; Mismatches 139;
                                                                                                                                                                                       Brain Res. Mol. Brain Res. 43:30-40(1996).
                                                                                              SEQUENCE FROM N.A.
STRAIN-DBA/21bg;
MEDLINE-97189245;
PARTINE-97189245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 47.1
Matches 243; Conservative
                                      musculus (Mouse)
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                            STRAIN-DBA/21bg;
                                                                                                                                                                                                                                        Stitzel J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 TFHTHVLVHYSGSCQYIPPGILKSTCYIDVRWFPFDVQKCDLKFGSWTHSGWLIDLQMLE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 FMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ADISNYISNGEWDLVGVPGKRNELYYECCKEPYPDVTYTITMRRRTLYYGLNLLIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 LCLLWP-----RGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 VDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 TYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----CCRYYRGGEENG
                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last sequence update)
Alpha8 subunit of nicotinic acetylcholine receptor precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                               MEDLINE-90315158; PubMed-2369519; Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.; Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.; Brain alpha-bungarotoxin-binding protein cDNAs and mABs reveal subtypes of this branch of the ligand-gated ion channel gene superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.8%; Score 1219.5; DB 13; Lengt
46.3%; Pred. No. 3.9e-107;
iive 88; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10F362D153EC87A7 CRC64;
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                          494
459 DWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
              :||||| ||||||||||:||||| ::||||| ::
EWKFAACVVDRLCLMAFSVFIICTIGILMSAPNFV
                                                                                                511 AA
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Matches 236; Conservative
                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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Q03481
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                 208 ELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPP
                                                                                                                     268 DSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILN
                                                                                                                                                                                                                                            388 ANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLIL-----KEIRV
152 GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG----DISSFVTNGEW
                                                                                                                                                                                                                                                                                                                         443 ITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                             326 LHFRSADSHEMNPLVRRVLLEFLPWLLFMSRPG-----
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 15:14:55; Search time 10.386 Seconds (without alignments) 2245.843 Million cell updates/sec Run on:

US-09-303-232-4 2665 1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHIMVS 496 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	0 qa	homo sa	mus m	_	31 bos taurus		66 manduca sex		homo			78 drosophila		63 bos taurus		drosop		homo sa	l gallus	gallus	torpedo					10 torpedo cal		90 rattus norv	09 bos taurus	43 rattus norv	62 drosophila	80	56 mus musculu
	esc	227	P3654	P49582	055	P5413	481	P91766	234	P32297	015822	004	094	P12389	072	047	176	P0947	01582	094	P0948	027	P09482	305	P17787	P12392	P02710	P1884	P12390	P02709	P431	P251	P25108	P047
SUMMARIES		CHICK	_HUMAN	MOUSE	_RAT	_BOVIN	CAEEL	_MANSE	SCHGR	IUMAN	IUMAN	HICK	MΕ		IN		ME								N	RAT	TORCA	CARAU	RAT	BOVIN	RAT	DROME	RAT	MOUSE
	QI.	ACH7			ACH7	-	-														-		_											ACHA
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	Juery Match Length								557											496	491	461	622	498	502	495	. 461	512	200	457	493	519	457	457
ď	Query Match	47.5	46.8	46.6	46.2	45.7	45.1	36.8	36.7	36.0	36.0	36.0	35.9	35.7	35.1	34.9	34.7	34.5	34.4	4	34.1	4	m	ë.	e.	33.8	33.7	m.	33.7	ĸ.	33.6	۳.	33.4	33.4
	Score	12	1246	1241	1232.5	1218.5	1201	980.5	979	096	096	959	956.5	951	936.5	930	926	918.5	918	917	908.5	906	904	903.5	902.5	905	899	898.5	868	896.5	896.5	893.5	830	883
	Result No.	-	8	m	4	ß	Q	7	œ ·	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	. 58	29	30	31	32	33

P26153 gallus gall	P49581 gallus gall	P19370 carassius a	Q98880 brachydanio	P43681 homo sapien	P05377 xenopus lae	P04755 drosophila	P45963 caenorhabdi	P09483 rattus norv	P02708 homo sapien	P20420 rattus norv	Q05901 homo sapien	
ACHP_CHICK	ACH6_CHICK	ACHN_CARAU	ACHA_BRARE	ACH4_HUMAN	ACH2_XENLA	ACH3_DROME	ACH8_CAEEL	ACH4_RAT	ACHA_HUMAN	ACH5_RAT	ACHO_HUMAN	
~	-	Н	Н	-	Н	Н	_	1	П	П	7	
470	464	459	456	627	457	521	538	630	482	452	458	
33.3	33.3	33.2	33.0	33.0	32.9	32.8	32.7	32.6	32.5	32.2	32.1	
888	886.5	885.5	880	879.5	876.5	874	872	867.5	866.5	858.5	855.5	
34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 ACHICK ACHICK ACHICK ACHICK ACHICK ACHICK ACHICK ACHICK ACHICK DJ 01-AU DJ

LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120

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1 MGLRALMLWLLAAAGLV-----RESLQGEFQRKLYKELLKNYNPLERPVANDSQPLT

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121 LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT

181 YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK 240

241 İLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA 300

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN
'Mutations in the channel domain alter desensitization of a neuronal
                                                                                                                                                                                                                                                                                        SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SUBCELLULAR LOCATION: Integral membrane protein.
DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
IN THE DEVELOPING OPPITG TECTUM BETWEEN E5 AND E16.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                   FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                              MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC. MEDLINE-93024917; PubMed-1383829; Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S., Changeux J.-P., Bertrand D.; "Mutations in the channel domain of a neuronal nicotinic receptor convert ion selectivity from cationic to anionic."; Nature 359:500-505(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L->S,T: SUPPRESSES INHIBITION BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LIKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1267; DB 1; Length 502;
; Pred. No. 6.8e-100;
83; Mismatches 144; Indels 36;
                                                                                                                                                                                                                                                        SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHABUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPEN-CHANNEL BLOCKER QX-222
QR -> ET (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572325D4309AD2FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ransmembrane; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPHA-7 CHAIN.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X52295; CAA36543.1; -. EMBL; X68246; CAA48317.1; -. EMBL; X68586; CAA48576.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 48.6 Matches 249; Conservative
               nicotinic receptor.";
Nature 353:846-849(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502
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PDB; 1KL8; 17-APR-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JN0113
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502 AA;
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                                                                                                                                                                                                                                            MEMBRANE.
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301 VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG 360

463 AAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494

463

POCCRYYRGG--EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKF

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E-----DKVRPACQHKQRRCSLSSMEMNTVSGQQCSNGNMLYIGFRGLDGVHCTPTTDS 403

SATTPPPARVPPPDLELRERSSKSLLANVLD----

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Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.; "Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-Sx5x cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers
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                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
              P36544; 015826; Q96RH2; Q99555; Q9BXH0; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1997 (Rel. 39, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Neuronal acetylcholine receptor protein, alpha-7 chain precursor. CHRNA7 OR NACHRA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Logel J., Drebing C., Barnhart M., Antle C., Leonard S., Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
502 AA
  PRT;
                                                                                                                                                                                                                                                                                 MEDLINE-94195283; PubMed-8145738;
                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Pharmacol. 45:546-554(1994).
                                                                                                                                                                                                                                                                                                                                                                                        expressed in Xenopus oocytes
  STANDARD;
                                                                                                                                             Homo sapiens (Human).
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  HUMAN
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Gaps

U62436; AAB40114.1; -. Y08420; CAA69697.1; -. AF385585; AAK68111.1;

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us-09-303-232-4.rsp

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MIM; 118511; -

R GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.
R GO; GO:0004899; F:nicotinic acetylcholine-activated cation-se. .; TAS.
R GO; GO:000087; P:activation of MAPK; TAS.
R GO; GO:0006832; P:small molecule transport; TAS.
R InterPro; IPR006029; Neu_channel_memb.
R InterPro; IPR006029; Neu_channel_memb.
R InterPro; IPR006020; Neu_channel_memb.
R Pfam; PF02931; Neur_channel.
R Pfam; PF02931; Neur_channel.
R Pfam; PF02931; Neur_channel.
R Pfam; PF02931; Neur_channel.
R Pfam; PF02932; Neur_channel.
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R Pfam; PF02931; Neur_channel.
R Pfam; PF02931; Neur_channel.
R TIGRPAM; TIGRPAM: TIGNCHANNEL.
R TIGRPAM; TIGNCHANNEL.
R PROSITE; PS00236; NEUROTE_ION_CHANNEL; 1.
R PROSITE; PS00236; NEUROTE_ION_CHANNEL; 1.
R PASSITE; PS00236; NEUROTE_ION_CHANNEL; 1.
R TABSSEMEMBERANE.
M POSTASYNAPIAN; SIGNAL; SIGNAL; TANSSEMEM PASSITE; PS00236; NEUROTE_ION_CHANNEL; 1.
                                                          EMBL; L25827; -; NOT_ANNOTATED_CDS.
EMBL; 223141; CAA80672.1:
                                                                                                                                   EMBL; AF33258; AAR19515.1;
PIR; GO2259; GO2259;
PIR; 137185; ACHUA7.
Genew; HGNC:1960; CHRNA7.
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                                          MEDLINE=97162233; PubMed-9009220; Groot Kormelink P.J., Luyten W.H.M.L.; Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAchR) subunits beta3 and beta4 and expression of seven nAchR subunits in the human neuroblastoma cell line SH-SY5X and/or IMR-32."; FEBS Lett. 400:309-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and chromosomal localization of the human alpha 7-nicotinic receptor subunit gene (CHRNA7).";
Genomics 19:379-381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riley B., Williamson M., Collier D., Wilkie H., Makoff A.; "A 3-Mb map of a large segmental duplication overlapping the alpha7-nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14."; Genomics 79:197-209(2002).
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MEDLINE-21829512; PubMed=11840567;
MEDLINE-21829512; PubMed=11840567;
MEDLINE-21829512; PubMed=11840567;
Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
Zvelebil M.J.;
Cluster analysis of an extensive human breast cancer cell line
Protein expression map database.";
Protein expression map database.";
Proteonics 2:212-223(2002).
I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONPORMATION THAT APPECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T., Lee J., Tian J., Giordano T.; "Cloning and sequence of the human a7 nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.
MASS SPECTROMETRY: MW-54157.68; METHOD-MALDI.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti M.,
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                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Epidermal keratinocytes;
Arredondo J., Grando S.A.;
"Cloning cholinergic receptors in human keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                 Groot Kormelink P.J., Luyten W.H.M.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
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MEDLINE-21818878; PubMed-11829490;
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NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN.

SIMILARITY.

EXTRACELLULAR (POTENTIAL)

POTENTIAL. POTENTIAL ASSOCIATED WITH RECEPTOR ACTIVATION

CYTOPLASMIC (POTENTIAL)

POTENTIAL. BY SIMILARITY.

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(BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

A -> G (IN REF. 1 AND 7).

S -> N (IN REF. 2 AND 6).

S -> P (IN REF. 2 AND 6).

C -> S (IN REF. 9 AND 6).

A -> G (IN REF. 1).
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D94B3A482EAA0E42 CRC64;
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                                                                                                                                                        56449 MW;
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Matches 240; Conservative
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502 AA;
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EMBL; X70297; CAA49778.1; -.

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Q05941;
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CARBOHYD
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393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                 ----VPPPPDLELRERSSKSLLANVLD
                                                        ORRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
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ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 acetylcholine receptor.";
Genomics 26:399-402(1995).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c; TISSUE-Brain;
MEDLINE-95324936; PubMed-7601470;
Orr-Urtreger A. Seldin M.F., Baldini A., Beaudet A.L.;
"Cloning and mapping of the mouse alpha 7-neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
POSTSynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALI
BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                   DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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                                                                                                                                                                                                                      502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L37663; AAC42053.1; -
PTR; A57175; A57175.
MGD; MGI:99779; Chrna7.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
Fam; PF02931; Neur_chan_LBD: 1.
PFam; PF02932; Neur_chan_LBD: 1.
PRINTS; PR02952; NEURONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                  -----SATTPPPAR-----
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                               (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                             -DEHLLH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
231
                                                                                                                                                                                                                                                                                              CHRNA7 OR ACRA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBRANE.
                                                                                                                                                                                                                                             01-FEB-1996
                                                                                                                                                                                                                     ACH7_MOUSE
P49582;
                                                                                                                                                          453
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TRANSMEM
                                  361
                                                                                                         417
                                                                                                                                   453
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                                                                                                                                                                                                           ACH7_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                       LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120
                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                 52
                                                                                                                                                                                                                                                                                                                                 LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDKVRPACOHKP------RCSLASV-ELSAGAGPPTSNGNLLYIGFRGLEGMHCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 VPLIAQYFASTMIIVGLSVVVTVIVLRYHHHDPDGGKMPKWTRIILLNWCAWFLRMKRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGE----
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                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.; Molecular cloning, functional properties, and distribution of rat brain alpha 7: a nicotinic cation channel highly permeable to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1998 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
CHRNA7 OR ACRA7.
                                                                                          ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                           (b) SIGLANDIA).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                    DB 1; Length 502;
                                                                                                                                                                                                                                                Pred. No. 1.1e-97;
90; Mismatches 139; Indels
                                                                                                                                                                                             C9312E5226D120E3 CRC64;
                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||||| |||||||: |::|||| |: :||||| : EWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                  Score 1241; DB 1;
Pred. No. 1.1e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                        POTENTIAL.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93147931; PubMed=7678857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                             MM;
                                                                                                                                                                                                                                  46.68;
                                                                                                                                                                                           56631
                                                                                                                                                                                                                      Query Match
Best Local Similarity 47.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
280
317
469
490
164
213
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90
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133 1
502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
262
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212
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Name=Short;
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                                                                                                                                                                                                                                                                                                                                                   ACH7_BOVIN
             122
                                                                                                                                                                                                                                                    399
                                                                                                                                                                                                                                                                                                                                                                                                                  CHRNA7
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                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGR------GGIWLALAAALLHVSLQGEFQRRLYKELVKNYNPLERPVANDSQPLTV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                  itted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                              SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                       SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
POSTSYnaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 5.8e-97;
83; Mismatches 141; Indels
                                                     Boulter J.; Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00996E74EC7B9A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N -> F (IN REF. 2).
P -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.2%; Score 1232.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                     EMBL: L31619; AAC33136.1; -...
PIR: T01378; T01378.
InterPro: IPR0066029; Neu_channel_memb.
InterPro: IPR0066201; Neur_channel.
InterPro: IPR006201; Neur_channel.
Pfam: PF02931; Neur_chan_LBD.
Pfam: PF02931; Neur_chan_memb; 1.
Pfam: PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                              STRAIN-Sprague-Dawley; TISSUE=Brain;
                                            STRAIN-Sprague-Dawley; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fransmembrane; Multigene family SIGNAL 1 22 BY
          Neurosci. 13:596-604(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
90
133
N 447
469
56410 MW;
                                                                                                                                                                                                                                                                                                                            EMBL; S53987; AAB25224.2; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 244; Conservative
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255
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502 AA;
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                               SEQUENCE FROM N.A.
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231
262
296
318
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150
212
                                                                                    REVISION TO 363
                                                                                                          Hartley M.
Submitted
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TRANSMEM
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TRANSMEM
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 DKVRPACQHKPRRCSLASVELSAGAGPPTSN------GNLLYI--GFRGLEGMHCA 398
MYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                       PLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 PQAQQPQCCRYYRGGEENGAGL--AAHSCFGVDYELSLILKEIRVITDQMRKDDEDADIS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTPDSGVVCGRLACSPTHDEHLMHGAHPSDG-DPDLAKILEEVRYIANRNRCQDESEVIC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY STRUCTURE), HOWO-OLIGOMER OF THE SHORT FORM GIVES RISE TO UNFUNCTIONAL CHANNELS, AS DOES COEXPRESSION OF BOTH LONG AND SHORT FORMS OF THE RECEPTOR.
                                                                                                                                                                                                                                                                                          242 LYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV
                                                                                                                                                                                                                                                                                                                                DGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKT
                                                                                                                                                                                       "Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine chromaffin cells: molecular cloning, functional expression and allernative splicing of the alpha 7 subunit.";

Eur. J. Neurosci. 7:647-655(1995).

-!-FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-07T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isod=P54131-2; Sequence=VSP_000075; Isod=P54131-2; Sequence=VSP_00075; IISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Adrenal meduila;
MEDLINE-95346009; PubMed-7620615;
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEWKFAACVVDPLCLMAFSVFIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 RDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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NCBI_TaxID=9913;
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                                                                                       62 VDEKNQVLTTNIWLQWIWTDHYLQWINASEYPGVKTVRFPDGQIWKPDILLYNSADERFDA 121
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N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

MISSING (in isoform Short).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 1218.5; DB 1; Length
46.1%; Pred. No. 8.9e-96;
Live 80; Mismatches 115; Indels
                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
MEDLINE-86194078; PubMed-8627624;
Ballivet M., Alliod C., Bertrand S., Bertrand D.;
"Nicotinic acetylcholine receptors in the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Bristol N2;
Nelson J., Wohldmann P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
-!- SUBCELLULAR LOCATYON: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_LBD; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGREMAS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PROSITE; PS0x19xpaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETYLCHOLINE RECEPTOR LIKE
                449 ESEAVCSEWKFAACVVDRLCLMAFSVFTILCTIGILMSAPNFV 491
452 EDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA-TYPE CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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InterPro; IPR006202; Neu_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
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[2]
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PIR, S68588; S68588.
HSSP; P58154; 1198.
WormPep; F25G6.3; CE09639.
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                                                                                                           STANDARD;
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                                                                                                           ACH1_CAEEL
P48180;
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                                                                                                                                                       NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG 196
                                                                                                                                                                                                                                              SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVA 316
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                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
NCBI_TaxID=7130;
                                                                                                                                                                                                                                                        245 LMTLLGFTLPPDAGEKITLQITVLLSICFFLSIVSEMSPPTSEAVPLLGIFFTCCMIVVT
                                                                                                                         NQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPT
                                                                                                                                                                                                  DISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIA
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                                                                17 LLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEK
                                                                                     LLISCAILAAPTLGSLQERRLYEDLMRNYNNLERPVANHSEPVTVHLKVALQQIIDVDEK
                                                                                                                                                                                                                                                                                                                                   PPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQC-CRYYRGGEENGAGLAA-----
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENT. J. NEUROSCI. 10:879-889(1998).
-I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain precursor (MARA1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P., Reynolds S.E., Wolstenholme A.J., Wonnacott S.; "Characterization of a nicotinic acetylcholine receptor from the insect Manduca sexta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                             30;
                                           89; Mismatches 151; Indels
                        Length
 E463ABB40AC9FA82 CRC64;
                     Score 1201; DB 1;
Pred. No. 2.7e-94;
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FTIFIIVSTIGIFWSAPYLV 497
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57169 MW;
                       45.18;
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                                             Conservative
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                                al Similarity
230; Conserv
498 AA;
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P91766;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL). 67; 1. channel; Glycoprotein; 36.8%; Score 980.5; DB 1; Length 516; 40.5%; Pred. No. 1.5e-75; Live 75; Mismatches 159; Indels 67 MVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP-N-LINKED (GLCNAC. . .) (PC E7A71E8C45D13BD2 CRC64; EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL) POTENTIAL. BY SIMILARITY InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006029; Neu_chan_LBD.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRNS; PF00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSTIE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic changes. 373 VTGAGETTLWDEGSPGVPAPPRPPPCAPP-466 VVDRLCLIIFTLFTIIATLAVLLSAP 491 POTENTIAL. POTENTIAL 30.0 40.5%; Fin Fransmembrane; Multigene family 58720 MW; EMBL; Y09795; CAA70928.1; -. Conservative 45 132 516 45 132 233 516 AA;

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462 VLDRPFLWIFTLAVVVGSAGIILQAP 487

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PRINTS; PR00252; NRIONGHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROPT ION.CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
                                                                                                                                                                                                                                                  MEDLINE-91092263; PubMed-1702381; Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W., Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Gosey M.W., Darlison M.G., Sattelle D.B., Barnard E.A.; "Sequence and functional expression of a single alpha subunit of an
                                                                                                                                                                                                                                                                                                                                                      FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                  Schistocerca gregaria (Desert locust).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acriddidae; Cyrtacanthacridinae; Schistocerca.

NCBL_TaxID=7010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.7%; Score 979; DB 1; Length 557; 40.0%; Pred. No. 2.2e-75; ive 88; Mismatches 160; Indels
                                                                                01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-Ll chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168389C887DFDF3E CRC64;
                                 557 AA
                                                                                                                                                                                                                                                                                                                        insect nicotinic acetylcholine receptor."; EMBO J. 9:4391-4398(1990).
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HIS-RICH.
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                 PRT.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Multigene family
                                                              01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63026 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X55439; CAA39081.1; +. PIR; S12359; S12359.
                                STANDARD;
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Matches 217; Conserv
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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330
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                              ACH1_SCHGR
P23414;
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DOMAIN
SEQUENCE
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RESULT 8
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10;

Gaps

78;

Conservative

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243 YYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVP 302
                                                                                                                                                                                                                                                                                                                                                           71 IDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGF 130
                                                                                                                                                                                                                                                                                   LLGTYFNCIMFWVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSA 362
                                                                                                                                                                                                                                                                                                                                        363 TTPPPARVPPPDLELRERSSKSLL--------ANVLDIDDDFRHPQ 401
                                                                                                                                                                                                                                                                                                                                                                                                                           409 LHQHQHHHQLHHLQRPGGCNGLHSATNRFGGSAGAFGGLPSVVGLDGSLSDVATRKKY 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
                            63
                11 AAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQI
                                                                                                                DSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL--
                                                                                                                                                                      --QLQDEG----GGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTL
                                                                                                                                                                                                                                                                                                  coding for the alpha 3 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P32297; 015823; 096RH3; 099553; 098093; 01-0CT-1993 (Rel. 27, Created) 01-NOV-1997 (Rel. 35, Last sequence update). 15-SEP-2003 (Rel. 42, Last annotation update) Neuronal acetylcholine receptor protein, alpha-3 chain precursor. CHRNA3 OR NACHRA3.
                                                                                                                                                                                                                                                                                                                                                                                                402 AQQPQCCRY-----YRGGEENGAGLAAH-------SCFGVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90245296; PubMed-2336208;
Fornasari D., Chini B., Tarroni P., Clementi F.;
"Molecular cloning of human neuronal nicotinic receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE-97062879; PubMed-8906617;
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 AA.
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"Expression of mRNAs in human thymus
of a neuronal acetylcholine receptor.
Exp. Neurol. 111:175-180(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Thymus;
MEDLINE=91114756; PubMed=1989896;
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A propleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Nilating M.M. Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=97162233; PubMed=9009220;
Groot Kormelink P.J., Luyten W.H.M.L.;
"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven mAChR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32.";
FEBS Lett. 400:309-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99118870; PubMed-9921897; Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.; "The Structures of the human neuronal nicotinic acetylcholine receptor beta2- and alpha3-subunit genes (CHRNB2 and CHRNA3)."; Hum. Genet. 103:645-653(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.; "Characterization of the human beta4 nAChR gene and polymorphisms in CHRNA3 and CHRNA4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arredondo J., Grando S.A.;
"Cloning cholinergic receptors in human keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER BINDING ACCTYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M., "Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anand R., Lindstrom J.;
Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT LEU-21 INS.
MEDLINE=21342809; PubMed=11450844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                          beta 4 subunits.";
J. Mol. Neurosci. 7:217-228(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hum. Genet. 46:362-366(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 6-493 FROM N.A.
TISSUE-Epidermal keratinocytes;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMBRANE.
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Event-Alternative splicing; Named isoforms=2;

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R GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.
R GO; GO:0005892; C:nicotinic acetylcholine-activated cation-se. .; TAS.
R GO; GO:0005812; F:transporter activity; TAS.
R GO; GO:0007165; P:signal transduction; TAS.
R GO; GO:0006832; P:signal transduction; TAS.
R GO; GO:0006832; P:signal transport; TAS.
R GO; GO:0006832; P:signal transport; TAS.
R InterPro; IPR006202; Neu_channel_memb.
R InterPro; IPR006202; Neu_channel.
R Ffam; PF02931; Neu_chan_memb.
R Pfam; PF02932; Neu_chan_memb.
R Pfam; PF02032; Neu_chan_memb.
R Pfam; PF02032; Neu_chan_memb.
R Pfam; PF02032; Neu_channel.
R RGFAMS; TIGR00860; LIC; II.
R Receptor; PS01036; NEUROTR_LOW_CHANNEL.
R Receptor; PS01036; NEUROTR_LOW_CHANNEL.
R Receptor; PS01036; NEUROTR_LOW_CHANNEL; II.
R Receptor; PS01036; Neurorane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family; Alternative splicing; POlymorphism.
T SIGNAL
                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                        Note=No experimental confirmation available;
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N.E. SIMILARITY).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

MALAN -> MGSCPL (In isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSLPLALSP -> ALAAPGAVA (IN REF. 2).
LSPP -> CRA (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8A9EBC5D71AEC7D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD -> TT (IN REF. 1).
I -> S (IN REF. 1).
L -> V (IN REF. 1).
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VSLPLALSP -> ALA
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            IsoId=P32297-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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BY SIMILAR
                                                                                                                                                                                                             EMBL, M86383; AAC84176.1, --
EMBL, M37981; AAA59942.1; --
EMBL, W06418; CAA65942.1; --
EMBL, Y08418; CAA69695.1, --
EMBL, AJ007784; CAA07682.1; --
EMBL, AJ007784; CAA07682.1; JOINED.
EMBL, AJ007785; CAA07682.1; JOINED.
EMBL, AJ007785; CAA07682.1; JOINED.
EMBL, AJ007785; CAA07682.1; JOINED.
EMBL, BC001642; AAH01642.1; --
EMBL, BC002996; AAH01642.1; --
EMBL, AF385584; AAK68110.1; --
EMBL, X55559; CAA37625.1; --
EMBL, X55559; CAA37625.1; --
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14 L6
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100 D
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MIM; 118503; -.
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                                         IsoId=P32297-2;
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PIR; A53956; A53956.
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503 AA;
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                           Name=2
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TRANSMEM
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CARBOHYD
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                                                              12 APAGLILLICLLUNPRGARCGYHEKRILHHILDHYNVLERPVVNESDPLQLSFGLTLMQII 71
                                                                                                                                              VDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGSWSYDKAKIDLVLI
                                                                                                                                                                                                                                                                          G-SSMNLKDYWESGEWAIIKAPGYKHDIKYNCCEEIYPDITYSLYIRRLPLFYTINLIIP
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                                                                                            SPPRLLLLLLLSLLP-VARASEAEHRLFERLFEDYNEIIRPVANVSDPVIIHFEVSMSQLV
                                                                                                                             DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                                                                           STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
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MEDLINE-97062879; PubMed-8906617;
Bliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic accetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FIB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
                               30;
 503;
Score 960; DB 1; Length 50
Pred. No. 7.9e-74;
); Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Groot Kormelink P.J.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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. Neurosci. 7:217-228(1996)
                               90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 IFTLFTIIATLAVLL 488
36.0%;
41.0%;
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480 VFTLVCILGTAGLFL 494
                               Matches 203; Conservative
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                Similarity
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Blechschmidt K.,
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Q15822; Q9HAQ3;
01-NOV-1997 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                     SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE COMBINED TO BETA-4 TO GIVE·RISE TO FUNCTIONAL RECEPTORS. SUBCELLUIAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLILMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN.
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!-, FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

7F512B06CCD9AAFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                          ; ILBOUZ; -: C. Intootinic acetylcholine-gated receptor-chan. GO:00004889; F:nicotinic acetylcholine-activated cation-se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.0%; Score 960; DB 1; Length 52
38.9%; Pred. No. 8.4e-74;
iive 90; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0007268; P:synaptic transmission; TAS.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neu_chan_LBD.
Ffam; PF02931; Neu_channel.
Ffam; PF02931; Neu_chan_LBD; 1.
PF137; PF02932; Neu_chan_LBD; 1.
PRINTS; PR00252; NRIONCHANNEL.
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POTENTIAL.
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BY SIMILARITY
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CYTOPLASMIC.
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EMBL; Y16281; CAA7G154.1; -.
EMBL; AF311103; -; NOT_ANNOTATED_CDS.
Genew; HGNC:1956; CHRNA2.
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199; Conserv
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                                                                                                                                                                                                                                                                                                                        Genew; HGNC::
MIM; 118502;
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243

184 YQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLY

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363
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                                                                                                                                                                                                                                                                                                                                     --HPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADI
                                                                 YFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                           - | | | : | | | : | | : : | | : : | | : : | | : : : | | : : | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : : | | | : : : : | | | : : : | | | : : : : | | | : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | : : : | | | : : : : | | | : : : | | | : : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : : | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : : | | | | : : : | | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | | : : : | | | : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Last Sequence update)
28-FEB-2003 (Rel. 11, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA), A FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND THREE NON-ALPHA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.; "Genes expressed in the brain define three distinct neuronal nototinic acetylcholine receptors."; EMBO J. 7:595-601(1988).
                                                                                                                                                                                                                                            TPPPARVPPPDLELRERSSKSLLANVLD-----IDDDFR-----
                                                                                                                                                                                                                                                                                                                                                                                                                            SRDWKFAAMVVDRLCLIIFTLFTIIATLAVLL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                      490 KEDWKYVAMVIDRIFEWLFIIVCFLGTIGLFL 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       528 AA
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InterPro; IPR006029; Neu_channel_memb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=88283624; PubMed=3267226;
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EMBL; X07341; CAB59645.1; JOINED.
EMBL; X07342; CAB59645.1; JOINED.
EMBL; X07343; CAB59645.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X07344; CAB59645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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P09480;
                                                               244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 GKASGGPAPQVPLKGEEVGSDQGLTLSPSILRALEGVQYIADHLRAEDADFSVKEDWKYV 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 GFAEDRLFKHLFTGYNRWSRPVPNTSDVVIVKFGLSIAQLIDVDEKNOMMTTNVWLKQEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 EKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP-----PPPDLELRERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 SRCWLET - - DVDDKWEEEEEEEEEEEEEERAYPSRVPSGGSO - - - GTQCHYSCERQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKSLLANVLDIDDDFRHPQAQQPQ------CCRYYRGGEENGAGLAAH-SC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 RSPSTHTMPHWVRSFFLGFIPRWLFMKR-----PPLLLPAEGTTGQYDPPGTRL--ST
                                                                                                                                                                                                           NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BI SIMILARITI).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
E76C6360AF976364 CRC64;
              Pfam: PF0231; Neur_chan_EBD; 1.
PRIM: PF0231; Neur_chan_memb; 1.
PRIMTS: PR00252; NRIONGHANNEL.
TIGRPAMS: TIGRO0860; LIC; 1.
PROSTIE: PS00236; NROOPE, ION_CHANNEL; 1.
POSTSYNAPLIC membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.0%; Score 959; DB 1; Length 52:
39.2%; Pred. No. 1e-73;
Live 84; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACHI_DROME STANDARD; PRT; 567 AA. P09478; Q9VC74; 01-MAR-1989 (Rel. 10, Created) 15-SEP-2003 (Rel. 42, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                 ALPHA-2 CHAIN
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 AMVVDRLCLIIFTLFTIIATLAVLL 488
                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60675 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 36.0
Best Local Similarity 39.2
Matches 198; Conservative
                                                                                                                                                                                                                                                       239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 AA;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ra Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ra Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Gocayne B.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Burton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Aradon R.C., Rogers Y.-H.C., Blazej R.G., Channep M., Pfeiffer B.D., Ra Ballew R.M., Basu A., Baxendall J., Baytaktaroll C., Baldwin D., Ballew R.M., Basu A., Baxendall J., Baytaktaroll L., Beasley E.M., Ballew R.W., Bauch R.P., Borchan M.R., Bouch J., Botchan M.R., Bouch J., Botchan M.R., Bouch J., Botchan M.R., Bouch J., Botchan M.R., Dutler H., Cadleu E., Center A., Chadra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Andrews D., Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chadra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Andrews M., Doub L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodon K., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., Glodek A., Gong F. Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A., Havrey D., Helman T.J., Hernandez J.R., Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Moshrefi A., Jalli M., Kalush F., Karpen G.H., Kez J., Kennison J.A., Ketchum K.A., Jalli M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A., Jalli M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A., Jalli M., Malshina N.V., Mobarry C., Morley B., Moshrefi A., Mont M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G., Reinfert K., Wassarman D.A., Mixon K., Nusskern D.N., Nelson D., Millams S.M., Woodage T., Wonzley K.C., Wu D., Yang S., Yao Q.A., Walliams S.M., Woodes W., Sunger B., Spier E., Spradling R.N., Zhong W., Zhu S., Dun Y., Saith H., Walley B.C., Shand H., Stiener K., Wassarma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D. N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                systematic review.";
ecome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
                                                                                                                                                                                                                                                                   MEDLINE-88283626; PubMed-2840281;
Bossy B., Ballivet M., Spierer P.;
"Conservation of neural nicotinic acetylcholine receptors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome:
15-SEP-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha-like chain 1 precursor.
NACR-ALPHA-96AA OR ACRB OR ALS OR ACR96AA OR CG5610.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Ephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                 Drosophila to vertebrate central nervous systems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                                                                        EMBO J. 7:611-618(1988).
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=7227;
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PIR; $00381; ACFFA1.

FlyBase; FBqn0000056; nAcR-alpha-96Aa.

FlyBase; FRR006202; Neu_channel_memb.

InterPro; IPR006202; Neur_channel.

Ffam; PF02931; Neur_channel.

Ffam; PF02931; Neur_channel.

Ffam; PF02932; Neur_channel.

Ffam; PF029334; Neur_channel.

Ffam; PF02934; Neur_channel.

Ffam; PF02944; Neur_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ---EGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRKTLYYFFNLI
                                                                                                                DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
SIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-LIKE CHAIN 1. EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Y -> H (IN REF. 1).
                                                                                                                                                                 SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08E1F721FB2A92AC CRC64;
                                                                      membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.9%; Score 956.5; DB 1
38.2%; Pred. No. 1.8e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> H.
-> H (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
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                                                                    Integral memb
S IN EMBRYOS.
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                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X07194; CAA30172.1; -.
                                                                                               CNS
                                                                      SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                               TISSUE SPECIFICITY:
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538
108
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325
513
532
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108
567 AA;
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                                                                                                                                             LARVAE STAGES
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                                              MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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TRANSMEM
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  g
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DR Pfam DR Pfam DR Pfam		KW Tran						FT CARB		SQ SEQU	Query M Best Lo Matches	. 40	qq	Qy	QΩ	δŏ	. qa	Qy	qa	Qy	q 0	Qy	qa	Qy	q _Q	YQ .	qa	Qy	qa .	RESULT 14	ID ACH3 AC 0072 DT 01-0	
7 310 CIMEMVASSVVSTILILNYHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPAR 369 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	370 VPP	367 QPPEVLTDVYHLPPDVDKEVNYDSKRFSGDYGIPALPAŞHRFDLAAAGGISAHCFAEPPL 426	388 ANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDXELS 434 1	435 LILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIATLAVLLSAPHI 4	: : : : : :	RESULT 13	7							N MEDLINE-881/8113; PubMed=2882952; N Wada K., Balliver M., Boulter J., Connolly J.G., Wada E., Denorie F. C. Science J. Indicate F. C. Connolly J.G., Wada E.,				Boul	SUBMITCHER (UNT-1997) CO THE EMBLYGENBROK/DDBJ GATADABRES I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXPENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SIBHINITS AND		+	COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.				use by non-proint institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial		EMBL;	EMBL; M20292; AAA40664.1; EMBL; M20293; AAA40664.1;	EMBL EMBL EMBL	PIR; A40110; A40110. InterPro; IPR006029; Neu_c InterPro; IPR006202; Neur_	InterPro;
oy Pa	οy	q	Q D	Q	d d	24 4	i a	S T	555	G S	888	ואכ	× 62 6	* 6* 0	2 2 2	R R	5 P	. 04. 0	388 388	OO	υū	υί	000	טטכ	00	200	, 0 (ם מ	2 2 2	2 0 2	2	Ω

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 KNQMMTINVWLKQEWNDYKLRWDPAEFGNVTSLRVPSEMIWIPDIVLYNNADGEFAVTHM 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQDGGG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 SCLTVLVFYLPSECGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFV 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 LELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEEN---GAGLAAHSCFGVDY- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

ALPHA-2 CHAIN.

EXTRACELLULAR.

POTENTIAL.

POTENTIAL.

POTENTIAL.

CYTOPLASMIC.

POTENTIAL.

N-LINKED (GLCNAC. . .) (POTENTIAL).

C -> S (IN REP. 1; AAA40664).

MW; 3824E83BB01D613B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 GDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 ASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.7%; Score 951; DB 1; Length 511;
39.4%; Pred. No. 4.7e-73;
iive 90; Mismatches 167; Indels 48; Gaps
nm; PF02931; Neur_chan_LBD; 1.
an; PF02932; Neur_chan_memb; 1.
INTS; PR00352; NRIONCHANNEL.
SRFAMS; TIGR00860; LIC; 1.
SSITE; PS00326; NBUSNORY, LON_CHANNEL; 1.
SSITE; PR00326; NBUSNORY, LON_CHANNEL; 1.
STSYARDPIC membrane. Ionic channel; Glycoprotein; Signal; nismembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3. BOVIN STANDARD; PRT; 495 AA. 263; OCT-1994 (Rel. 30, Created)
OCT-1994 (Rel. 30, Last sequence update)
                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 VVDRIFLWLFIIVCFLGTIGLFL 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 VYDRLCLIIFTLFTIIATLAVLL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58611 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocal Similarity 39.4%;
s 198; Conservative
                                                                                                                                                                                                                                                                                        AIN
NSMEM
AIN
ULFID
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BOHYD
FLICT
UENCE
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NSMEM
NSMEM
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us-09-303-232-4.rsp

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PRT;
                                                                                                                                                                                                                                                                                           DRLCLIIFTLFTIIATLAVLL 488
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=88041184; PubMed=2444984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94193711; PubMed=8144606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHRNA3 OR ACRA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rrssue-Liver;
                                                                                                                                         305
                                                                                                                                                                                         361
                                                                                                                                                                                                                                           418
                                                                                                                                                                                                                                                                                           468
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                                                                                                                                                                                                                                                                                                                                                                                ACH3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patrick
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                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 SADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDORCEMKFGSWTYDGY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 ARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
PRINTS; PR00522; NEUROCHANNEL.
TIGRPAMS; TIGR00860; LIC; 1.
PROSTIE; PS00236; NEUROCH, ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                           Neurochem. Res. 17:281-287(1992).
-i- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                     SeQUENCE FROM N.A.

MEDLINE-92319195; PubMed=1620271;

Criado M., Alamo L., Navarro A.;

Criado M., Alamo L., Navarro A.;

"Primary structure of an agonist binding subunit of the nicotinic acetylcholine receptor from bovine adrenal chromaffin cells.";

acetylcholine receptor from bovine adrenal chromaffin cells.";

acetylcholine Res. 17:281-287(1992).
                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

(BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                         SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 936.5; DB 1;
Pred. No. 7.7e-72;
9; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA-3 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006029; Neu_channel_memb
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39.5%;
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Matches 198; Conservative
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163
214
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                                                                           Bovinae; Bos
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162
195 AA;
                                                                                       NCBI_TaxID=9913;
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263
296
319
468
149
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CARBOHYD
SEQUENCE
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TRANSMEM
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                                                                           Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-3 SUBUNIT CAN BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.F.,
                                                                                                                                                                  185 QLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYY
                                  GTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 NTQRPRPFYSAELSNLNCFSRIESKVCKEGYPCQDGL------CGYCHHRRAKISNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGLA-AHSCFGVDYELSL------ILKEIRVITDQMRKDDEDADISRDWKFAAMVV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of an acetylcholine receptor alpha 3 gene promoter and its activation by the POU domain factor SCIP/Tst-1.";
J. Biol. Chem. 269:10252-10264(1994).
-!- FUNCTION: AFTER BINDING ACCTYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patrick J.;
Isolation of a cDNA clone coding for a possible neural nicotinic
acetylcholine receptor alpha-subunit.";
Nature 319:368-374(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor
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Proc. Natl. Acad. Sci. U.S.A. 84:7763-7767(1987).
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Boulter J., Evans K., Goldman D.J., Martin G., Treco
Helnemann S.F.,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 IIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQ
                                                                                                                                                                                                                                                                                                                   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
1 25 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                            NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
               LOCATION: Integral membrane protein.
BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (PROBABLE).
D66C491E832B9C34 CRC64;
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                                                                                                                                                                                                                InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
Pfam; PR0252; Neur_chan_memb; 1.
TIGRNS; PR00252; NEUROWCHANNEL.
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56997 MW;
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                            SIMILARITY:
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414 TRSSSSESVNAVLSLSALSPEIKEAIQSVKYIAENMKAQNVAKEIQDDWKYVAMVIDRIF 473
------AAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLC 471
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ch completed: August 13, 2003, 15:26:11 time : 11.386 secs Search Job time

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 15:21:45; Search time 18.5263 Seconds (without alignments) 2574.698 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-303-232-4 2665 1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHINVS 496

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	nicotinic acetylch	alpha 7 neuronal n	nicotinic acetylch	nicotinic acetylch	nicotinic receptor	alpha-bungarotoxin	nicotinic acetylch	hypothetical prote			a)	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch										
SUMMAKIES	ID	JN0113	G02259	ACHUA7	A57175	T01378	JH0173	868588	T25671	T19622	T19862	S12359	A53956	ACCH2N	ACFFA1	A37040	A40110	860589	A24572	ACFFA2	ACCHAN	ACCHNN	ACCH4N	G02421	S10505	I50548	JH0174	T09289	ACRYA1	B37014 ·
	DB	7	~	П	7	7	7	~	7	7	~	7	7	-	-	~	7	7	~	Н	Н	-	-	7	~	~	~	~	7	7
	Length	502	502	505	502	502	511	498	461	260	542	557	. 503	528	267	203	511	495	499	576	456	491	622	498	502	461	503	494	461	512
	Query	7.5	9.9	9.9			5.8	5.1	2.8	8.	9.6	5.7	5.1	0.9	6.6	8.	8.9	5.1	0.0	34.7	4.5		3.9	9.9		3.8	8.	3.8	7.	3.7
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nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	probable nicotinic	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	hypothetical prote	nicotinic acetylch	nicotinic acetylch	hypothetical prote
B35721	ACBOA1	S12899	S13872	ACHUA1	A39218	149458	A24383	A30992	S14703	JC4021	A28529	T24724	ACFFNN	A26456	T23843
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495	457	200	457	457	470	445	457	517	459	627	457	468	521	625	565
33.7	33.6	33.5	33.4	33.4	33.3	33.3	33.2	33.2	33.2	33.0	32.9	32.9	32.8	32.8	32.6
868	896.5	892.5	890	688	888	887	988	988	885.5	879.5	876.5	875.5	875	874	869
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1. JN0113
	nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken N;Alternate names: alpha-bungarotoxin-binding protein alpha chain
	C;Species: Galius galius (Chicken) C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999 C:Anonesion: rmilis. runlis. capana. pastas. eaces
	Cyaccession: Juvils; Juvils; Signator, Ballso; Signator, M.C.; Bertrand, S.; Millar, N. S.; Bertrand, S.; Millar, N. S.; Millar, N. S.; Millar, M. S.; Milla
	Neuron 5, 847-856, 1990 A;Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is development
	A;Reference number: JN0113; MUID:91097796; PMID:1702646 A;Accession: JN0113
	A;Cross-references: GB:X68586; NID:g287756; PIDN:CAA48576.1; PID:g287757 A;Experimental source: white leghorn; brain
	R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
	A; Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtypes of t
	A;Reterence number: JH01/2; MU1D:90315158; PM1D:2369519 A;Accession: JH0172
	A; Molecule type: mRNA A: Residue: 1-502 < SCH>
	A; Cross-references: EMBL:X52295; NID:q63077; PIDN:CAA36543.1; PID:q63078
	A) Experimental source; brain A (Francisco)
	Nyacter Satatanshi, b.; netinaluez, m.c.; Noticolli, 1.; Balliver, m.; matter, c.m. EMBO J. 11, 4529-4538, 1992
	A; Title: Neuronal specificity of the alpha? Michinic acetylcholine receptor promoter
	A; Keletence mumber: Szgulg; MulD:95049204; FMLD:142556/ A:Accession: S28018
	A; Molecule type: DNA
	A.Cross-references: EMBL:X68246; GB:S49751; NID:q65319; PIDN:CAA48317.1; PID:q65320
	A; Experimental source: white leghorn; erythrocyte
	R;Conti-Tronconi, B.M.; Dunn, S.M.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.;
	A; Title: Brain and mussle nicotinic acceptable neceptors are different but homolog
	A;Reference number: A94055; MUID:85270494; PMID:3860855 A:Accession: R25738
	A; Molecule type: protein
	A; Resudues: L4-12), ET; L24-41, X', A3-45, X', A4, CCON. C:Comment: This acetvi-choline receptor is blocked by alpha-bungarotoxin and is locali
	C;Genetics:
	A;Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3 C:Superfamily: acetylcholine receptor
	C; Keywords: Drain; Jycoprotein; ion channel; neurotransmitter receptor; phosphoprote
	F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
	F;231-254/Domain: transmembrane #status predicted <tr1></tr1>
	F;296-317/Domain: transmembrane #status predicted (TR3)
-	F;4/U-488/DOMBin: transmembrane #status predicted <1R4>

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carbohydrate (Asn) (covalent) #status predicted
ling site: phosphate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                      36;
                                                                                                                                                          Length 502;
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F;46,90,133/Binding site: carbohydrate (Asn) (covalent) #status | F:365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #F:415/Binding site: phosphate (Thr) (covalent) #status predicted F:442/Binding site: phosphate (Tyr) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha 7 neuronal nicotinic acetylcholine receptor - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_c C; Accession: G02259 R; Leonard, S. Submitted to the EMBL Data Library, November 1995 A; Reference number: H00936 A; Accession: G02259 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                      Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.6%; Score 1242; DB 2; 46.0%; Pred. No. 2.8e-100;
                                                                                                                                                 Score 1267; DB 2;
Pred. No. 1.9e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-502 <LED>
A;Cross: references: EMBL:U40583; NID:g1125076; PIDN:
C;Superfamily: acetylcholine receptor
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                                                                                                                                                                                                                83;
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                                                                                                                                                    47.5%;
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Best Local Similarity 48.6%
Matches 249; Conservative
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Amap position: 15q14-15q14

A;Note: defects in this gene have been associated with mental retardation and schizop

C;Complex: the functional receptor molecule is a heteropentamer with two alpha chains
C;Complex: the functional receptor
C;Complex: the functional receptor
C;Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter recept
E;1-23/Domain: signal sequence #status predicted <1R1>
F;24-50/Domain: transmembrane #status predicted <7R1>
F;26-28/Domain: transmembrane #status predicted <7R2>
F;26-31/Domain: transmembrane #status predicted <7R3>
F;26-31/Domain: transmembrane #status predicted <7R3>
F;40-488/Domain: transmembrane #status predicted <7R4>
F;40-488/Domain: transmembrane #status predicted <7R4>
F;46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Released type: mRNA
A; Residues: 1-502 <PEN>
A; Residues: 1-502 <PEN>
A; Experimental source: brain neuroblastoma cell line SHSY-5Y
B; Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.
Genomics 19, 379-381, 1994
A; Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotini
A; Reference number: A54194; MUID:94245214; PMID:8188270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human Nicotinic acetylcholine receptor alpha-7 chain Nicotinate names: cholinergic nicotinate receptor alpha-7 chain c; species: Homo sapiens (man) c; pate: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999 C; Accession: 137185; A54194; S60309 R; Pengq, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J. M.; Gerzanich, V.; Anand, R.; Lindstrom, J. Mol. Pharmacol. 45, 546-554, 1994 A; Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subuniomers expressed in Xenopus oocytes.

A; Reference number: 137185
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E---ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTWRRRTLYYGLNLLIP
                                                                                                                                                                                                                                                                                                                                                                                                                               STYPTNVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
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                                                                                                                               DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
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A; Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>
A; Cross-references: GB: 223141; NID: 9457736; PIDN: CAA80672.1; PID: 9457737
                                                                                                                                                                                                                                                                                                                                                                                          312 MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
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C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Tal-reb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C; Accession: T01378
R; Seguela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
R; Seguela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
A; Title: Molecular cloning, functional properties, and distribution of rat brain alph A; Reference number: Z14310; MUID:93147931; PMID:7678857
A; Accession: T01378
A; Accession: T01378
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-502 <SEG>
A; Accessives: L502 <SEG>
A; Cross-references: Emain
C; Superimental source: brain
C; Superimental source: brain 9 112 180 172 240 229 300 289 360 349 415 æ 120 398 PIPDSGVVCGRLACSPTHDEHLMHGTHPSDGDPDLAKILEEVRYIANRFRCQDESEVICS 458 ---ENGAGLAAHSCFGV-----DYELSLILKEIRVITDQMRKDDEDADISR 458 121 113 F;150-164/Disulfide bonds: #status predicted

Db 193ADISNYISNGEWDLVGVPGKRNELXYECCKEPYPDVTYTITMRRRTLYYGLNLLIPC 249 253 VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIM 312	RESULT 7 S6858 Incotninc acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditi C;Species: Caenorhabditis elegans C;Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999 C;Accession: S68588; S57496 R;Ballivet, M.; Alliod. C; Bertrand, S.; Bertrand, D. J. Mol. Biol. 258, 261-269, 1996 A;Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans. A;Feference number: S68587; MUID:96196478; PMID:8627624 A;Accession: S68588 A;Accession: S68588 A;Actus: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-498 <bal> A;Cross-references: EMBL:X83887; NID:9872087; PIDN:CAA58764.1; PID:9872088 C;Superfamily: acetylcholine receptor C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra F;20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <m< th=""><th>Query Match 45.1%; Score 1201; DB 2; Length 498; Best Local Similarity 46.0%; Pred. No. 1.1e-96; Anismatches 151; Indels 30; Gaps 7; Qy 17 LLLCLLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDER 76 Db 6 LLISCAILAAPTGSLQBERRLYEDLMRNYNNLERPVANHSEPVTVHLKVALQQIIDVDER 65 Oy 77 NQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPT 136 Pl:: </th><th></th><th>QY 257 SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVA 316 </th></m<></bal>	Query Match 45.1%; Score 1201; DB 2; Length 498; Best Local Similarity 46.0%; Pred. No. 1.1e-96; Anismatches 151; Indels 30; Gaps 7; Qy 17 LLLCLLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDER 76 Db 6 LLISCAILAAPTGSLQBERRLYEDLMRNYNNLERPVANHSEPVTVHLKVALQQIIDVDER 65 Oy 77 NQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPT 136 Pl::		QY 257 SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVA 316
114 LYNSADERFDATFHTNULVNASGHCQYLPFGEKSSCYIDVRWFFFDVQCKLKFGSWSY 173 182 DGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRRIYYNCCPPEYIDITFAVVIRKT 241 184 185	Oy 458 RDWKFAAMVVDRLCLIFFLFTIATLAVLLSAPHIM 494 :	ance is similar to acetylcholine receptor alpha chains bungarotoxin binding proteins are localized to extrasynaptic pseudode etylcholine receptor receptor protein; transmembrane protein approach; transmembrane protein alpha-bungarotoxin binding protein alpha-2 chain #status predicted <imila #status="" (asn)="" (covalent)="" <imila="" predicted="" predicted<="" sequence="" td="" transmembrane=""><td>Query Match 45.8%; Score 1219.5; DB 2; Length 511; Best Local Similarity 46.3%; Pred. No. 2.7e-98; Acrossivative 88; Mismatches 131; Indels 55; Gaps 9; Qy 20 LCLLWPRGARGGYHEKRLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIID 72 Pred. No. 11 Pred. No. 11 Pred. No. 12 /td><td>QY 73 VDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPRRLWKPDVLMYNSADEGFDS 132 </td></imila>	Query Match 45.8%; Score 1219.5; DB 2; Length 511; Best Local Similarity 46.3%; Pred. No. 2.7e-98; Acrossivative 88; Mismatches 131; Indels 55; Gaps 9; Qy 20 LCLLWPRGARGGYHEKRLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIID 72 Pred. No. 11 Pred. No. 11 Pred. No. 12 Pred. No. 12	QY 73 VDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPRRLWKPDVLMYNSADEGFDS 132

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C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                            C; Accession: T19622
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C; Species: Caenorhabditis elegans
C; Accession: T25671
R; Gattung, S.; Maggi, L.
Submitted to the EMBL Data Library, February 1997
A; Reference number: Z20067
A; Reference number: Z20067
A; Reference number: Z20067
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-461 <GAT>
A; Residues: 1-461 <GAT>
A; Residues: September: Status Bristol N2; clone D2092
C; Conetics: Caenorhabditis Source: Strain Bristol N2; clone D2092
                       94 NLRWNTSDFGGVKDLRVP--PHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILN 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG----DISSFVTNGEW 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 YHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPPARVPPPDLELRERSSKSLL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLIL-----KEIRV 442
-----NRHSESLIRNIKDNEHSLSRANSFDADCRLNQYIMTQSVSNGLTSLGSIPSTM 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 ETKLFTDLLKGYNPLERPYQNSSQPLEVKIKLFLQQILDVDEKNQIVSVNAMLSYTWFDH 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 EKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDM
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                                                                                                                                                                                                                                                                                                                                                                                                                 A Map position: 1
A;Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 1141; DB 2; Length 4; Pred. No. 1.6e-91; 85; Mismatches 121; Indels
                                                                                                  ||:| |::|: |||::|
FTIFIIVSTIGIFWSAPYLV 497
                                                                                  FTLFTIIATLAVLLSAPHIM 494
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Best Local Similarity 46.2%;
Matches 218; Conservative 8
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hypothetical protein C31H5.3 - Caenorhabditis elegans

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submitted to the EMBL Data Library, April 1997
A; Reference number: 219153
A; Accession: T19622
A; Accession: T19622
A; Accession: T19622
A; Accession: T1962
A; Status: prediminary, translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-560 <WIL>
A; Residues: 1-560 <WIL>
A; Residues: Loso <WIL>
A; Reperimental source: Clone C31H5
C; Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LLLLLCLLWPRGARC-----GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQ
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                                                                                                                                                                                                                                                                                                                                                                                      Indels 122;
                                                                                                                                                                                                                                                                                                                                           Length 560;
                                                                                                                                                                                                                                                  A;Map position: 1
A;Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C;Superfamily: acetylcholine receptor
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                                                                                                                                                                                                                                                                                                                                       39.8%; Score 1060; DB 2; 37.6%; Pred. No. 2.5e-84; tive 96; Mismatches 142;
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R; Hembry, C.
submitted to the EMBL Data Library, March 1996
A; Reference number: Z19188
A; Accession: T19862
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 37.68
Matches 217; Conservative
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predicted

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Sep

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F;47,235/Binding site: carbohydrate (Asn) (covalent) #status
         F;501-523/Domain: transmembrane #status predicted <TM4>
                                                               36.7%;
                                                                                 Best_Local Similarity 40.0
Matches 217; Conservative
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C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C; Accession: 512359
R; Marshall, J; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.; EMBO J. 9, 4391-4398, 1990
A; Titles: Sequence and functional expression of a single alpha subunit of an insect nicot A; Reference number: 512359; MUID:91092263; PMID:1702381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein F:1-23/Domain: signal sequence #status predicted <SIG> F:4-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <WAIF:245-266/Domain: transmembrane #status predicted <TM1> F:274-295/Domain: transmembrane #status predicted <TM2> F:308-329/Domain: transmembrane #status predicted <TM3>
                                                                                                              A;Gene: CESP:C40C9.2
A;Map position: X
A;Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1;
C;Superfamily: acetylcholine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 PRVIYSKVMAESYVEDVVMTELNKYMQ------KACL----ELKNISSQTRAMRK 492
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 1-542 <WIL>
A;Cross-references: EMBL:270266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A;Experimental source: clone C40C9
C;Genetics:
                                                                                                                                                                                                                                                                                        93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 KQGSIKNGVGPGKPTDSVHPSEGLSLMKNIKLGRQQTIDFEYEFHVQHNHLMPVAPSEMT
                                                                                                                                                                                                                                                                                                                         30 EYRLLADLRHNYDPYERPVANASEPLVVSVKIYLQQILDVDEKNQVITLVAWIEYQWTDY
                                                                                                                                                                                                                                                                                                                                                            94 NLRWNTSDFGGVKDLRVP--PHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                       GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ------DEGGGDISSFVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLL-----GTYFNCIMFMVASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---RYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITD
                                                                                                                                                                                                                                                                                        34 EKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFT
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134 C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                   85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                              Length 542;
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                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                        136;
                                                                                                                                                                                                            39.6%; Score 1055.5; DB
40.5%; Pred. No. 5.9e-84
:ive 94; Mismatches 13
                                                                                                                                                                                                            Query Match 39.6's
Best Local Similarity 40.5's
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-557 <MAR>
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nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: No. 194 #sequence_revision 07-oct-1994 #text_change 20-Aug-1999
C;Accession: A53956; S21338
R;Mihovilovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A;Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuro A;Reference number: A53956; MUID:91114756; PMID:1989896
A;Accession: A53956
A;Accession: A53956
A;Reference number: A53956; MUID:91114756; PMID:1989896
A;Residues: 1-503 < MIH>
A;Residues: 1-503 < MIH>
A;Residues: 1-503 < MIH>
A;Residues: L503 < MIH>
A;Residues: Callastrom, J.
Submitted to the EMBL Data Library, June 1990
A;Description: Nucleotide sequence of the mature human nicotinic acetylcholine recept A;Reference number: S21338
A;Reference number: S21338
A;Residues: 30-503 < ANA>
A;Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C;Genetics:
                                                        10;
                                                                                                                                                                                                                           71 IDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357
                                                                                                                                                                                                                                                                                                                                                                         LLGTYFNCIMFWVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSA 362
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                                                                                                                                                                   63
                                                                                                                                                 DSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YELSLILKEIRVITDQMRKDDE-DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            --QLQDEG----GGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTPPPARVPPPDLELRERSSKSLL-------ANVLDIDDDFRHPQ
                                                           Gaps
                                                        78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SCFGVD--
                                                        Indels
                                                        88; Mismatches 160;
Score 979; DB 2;
Pred. No. 2.9e-77;
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10;

62;

90 90 150

270 269 329

380 426 435 463

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A: Introns: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3
C; Superfamily: acetylcholine receptor
C; Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra
C; L2L/Domain: signal sequence #status predicted <SIG>
F; 22-567/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted
F; 240-264/Domain: extracellular #status predicted <RMP
F; 240-264/Domain: transmembrane #status predicted <RML>
F; 272-390/Domain: transmembrane #status predicted <RML>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nicotinic acetylcholine receptor alpha-1 chain precursor - fruit fly (Drosophila mela C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S00381; A38801
R;Bossy, B.; Ballivet, M.; Spierer, P.
EMBO J. 7, 611-618, 1988
A;Title: Conservation of neural nicotinic acetylcholine receptors from Drosophila A;Reference number: S00381; MUID:88283626; PMID:2840281
A;Accession: S00381
                                                                                                                                                                                                                                                        271 EKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHH 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP-----PPPDLELRERS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW
                                                                                                                                                  NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                210 NAIGRYNSKKYDCCTEIYPDITFYFVIRRLPLFYTINLIIPCLLISCLTVLVFYLPSDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------FGVDYELSL-----ILKEIRVITDQMRKDDEDADISRDWKFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 RSPSTHTMPHWVRSFFLGFIPRWLFMKR------PPLLLPAEGTTGQYDPPGTRL--ST
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A;Residues: 1-567 <-BO2>
A;Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A;Note: 538-Tyr was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Rosidues: 1-567 - ROGS>
A;Cross-references: GB:X07194; NID:97575; PIDN:CAA30172.1; PID:97576
A;Accession: A38801
                            Length 528
                         ; DB 1;
1.5e-75;
                                                   Pred. No. 1.5e
84; Mismatches
                         36.0%; Score 959; 39.2%; Pred. No. 1
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A;Cross-references: FlyBase:FBgn0000036
A;Map position: 3R 96A
                                                                            Conservative
                         Query Match
Best Local Similarity
Matches 198; Conserv
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C. Superfamily: acetylcholine receptor.
C. Superfamily: acetylcholine receptor.
C. Reywords: glycoprotein; lon channel; neurotransmitter receptor; postsynaptic membrane;
C. F.1-23/Domain: signal sequence #status predicted <SIG>
C. 24-528/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <AMI>
C. 24-678/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <AMI>
C. 272-290/Domain: transmembrane #status predicted <TM2>
C. 272-290/Domain: transmembrane #status predicted <TM3>
C. 502-520/Domain: transmembrane #status predicted <TM4>
C. 54,104/Binding site: carbohydrate (Asn) (covalent) #status predicted
C. 222-223/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                             124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 AVGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGSWSYDKAK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLG 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 SANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYVAMVI 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----GS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTPPPARVPPPDLELRERS-SKSLLANVLDIDDDFRHPQAQQPQC--CRYYRGGEEN- 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418 GAGLA-AHSCFGVDYELSL-----ILKEIRVITDQMRKDDEDADISRDWKFAAMVV 467
                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nicotinic acetylcholine receptor alpha-2 chain precursor, neuronal - chicken
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: S00377
                                                                                                                                                                                                                                                                                                                                                                           :: |:: ||| ||:: ||:||| ||| ||:|| ||:|| SMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWNPSDYGGAEFMRVPAQKIWKPDIVLYNN
                                                                                                                                                                                                                                                                          10 LAAPAG----LLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGL
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A;Residues: 1-528 <NEF>
A;Cross-references: EMBL:X07339; NID:g62792; PIDN:CAB59645.1; PID:g6136914
                                                                                                                                                                                                  Gaps
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A;Title: Genes expressed in the brain define three distinct neuronal A;Reference number: S00376; MUID:88283624; PMID:3267226
A;Accession: S00377
                                                                                                                                                                                                34;
                                                                                                                                            Length 503;
                                                                                                                                                                                             89; Mismatches 172; Indels
                                                                                                                                            Score 962; DB 2;
Pred. No. 7.7e-76;
                         GDB:125219; OMIM:118503
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DRIFLWVFTLVCILGTAGLFL 494
                                           A; Map position: 15q24-15q24
C; Superfamily: acetylcholine receptor
C; Keywords: neurotransmitter receptor
                                                                                                                                                  36.1%;
                                                                                                                                                                   41.18;
                                                                                                                                                                      Best_Local Similarity 41.1
Matches 206; Conservative
GDB: CHRNA3
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  A; Gene:
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                                                                                                                                                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                                                                                                            78 OLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PAAAAAAADLSPTFEKPYAREME 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A) Cross-references: EMBL:X52239, NID:g177897; PIDN:AAC84176.1; PID:g177898 C:Superfamily: acetylcholine receptor C:Superfamily: acetylcholine receptor C:Superfamily: acetylcholine receptor; Expandas: neurotransmitter receptor; transmembrane protein F:1-28 Domain: signal sequence #status predicted <SIG>F:29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status pr
                                                                                                                                                                                                                                                                                                         18 LLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL----QLQD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---EGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLI
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                               F;326-513/Domain: intracellular #status predicted <INT>
F;514-532/Domain: transmembrane #status predicted <TM4>
F;45,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;149-163;222-223/Disulfide bonds: #status predicted
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                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                Indels
F;306-325/Domain: transmembrane #status predicted <TM3>F;326-513/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                             86; Mismatches 174;
                                                                                                                                                                                     DB 1;
                                                                                                                                                                                  35.9%; Score 957.5; DB 1
38.2%; Pred. No. 2.2e-75;
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Best Local Similarity 40.81
Matches 203; Conservative
                                                                                                                                                                                                              Best Local Similarity 38.2
Matches 206; Conservative
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A; Residues: 1-502 <FOR>
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                          FDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQ 189
                                                                                                                  VPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPARVPPPPDLELRERS-SKSLLANVLDIDDDFRHPQAQQPQC--CRYYRGGEEN-GAGL 421
  I I DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEG
                                                                                                                                                                                                                                                                                                     310 CIMFMVASSVVSTILILINYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----GSATTP
                                                                                                                                                                                  LODEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLI
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Human neuronal NAC

Wild-type human

Nicotinic acetylch

Mutant human alpha

Chimeric alpha7/5-

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Human neuronal nic
V274T variant huma
Mutant human alpha
Mutant human alpha
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Drosophila melanog
Modified acetylcho
Neuronal nicotinic
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Modified acetylcho
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Neuronal nicotinic
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Caenorhabditis ele
Caenorhabditis ele
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Human neuronal nic
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Human neuronal nic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. virescens acetyl-choline receptor protein from clone Hva7-1.
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AAW09021
ABB82430
                                                          AAB50015
AAB50016
AAB50017
AAW12369
AAB12824
ABP50018
AAB50018
AAB50018
AAB50018
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AAW09022
AAW44155
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AAW44156
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                                                                                                WPI; 2000-014207/02.
N-PSDB; AAZ24476.
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(FARB ) BAYER AG.
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 Neuronal alpha-bun
Drosophila melanog
Human neuronal nic
Neuronal nicotinic
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D. melanogaster ac
H. virescens acety
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                                                                                              (without alignments)
1809.483 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                      / SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/ SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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2665
1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHIMVS 496
                                                                                 August 13, 2003, 15:14:30; Search time 43.5088 Seconds
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                                                                                                                                                                                                                                                 1107863
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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AAY50816
ABB63683
AAW12368
ABB60432
AAW44153
AAW09025
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Gapop 10.0 , Gapext 0.5
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Searched:

Drosophila melanog Neuronal nicotinic Drosophila melanog

Human neuronal Human neuronal Human neuronal

Human neuronal nic

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DE19819829-A1
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                        This invention describes a novel nucleic acid (NA) encoding a nicotinic acety-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents; that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved iformation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
                                                                                                                                                                                                                                                                                           MGGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
                                                                                                                                                                                                                TLYYFFULIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLUMVAETMPATSDA
                                                                                                                                                                                                                                                                                                                                                                                                  VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTI
                                                                                                                                                                                                                                           LSFGLTLMQIIDVDEKNQLLITUIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV
                                                                                                                                                                                                                                                                                  LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
                                                                                                                                                                                                                                                                                                                       YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                       SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAG
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
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                                                                                                                                                              / Match 100.0%; Score 2665; DB 21; Length 496; Local Similarity 100.0%; Pred. No. 2.9e-258; les 496; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D. melanogaster acetyl-choline receptor protein from clone Da7
         26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY50814 standard; Protein; 770 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melanogaster
                                                                                                                                             496 AA;
          1a;
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insectlicide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615 DISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 LLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 SSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DLELRERSSKSLLANVLDIDDDFRH------PQAQQPQCCRYYR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGEENGAG------LAAHSCF--GVDYELSLILKEIRVITDQMRKDDEDADISRDW
                                                                                                                                                                                                                                                                              New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.4%; Score 1850; DB 21; 70.0%; Pred. No. 3.3e-176; ive 30; Mismatches 49;
                                                                                                                                                      Schulte T;
                                                                                                                                                                                                                                                                                                                                                          Example la; Page 12-14; 26pp; German
98DE-1019829
                                                  98DE-1019829
                                                                                                                                                      Oellers N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 70.0 nes 361; Conservative
                                                                                                                                                                                                   2000-014207/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                770 AA;
                                                                                                       (FARB ) BAYER AG
                                                                                                                                                                                                                              N-PSDB; AAZ24475
                                                                                                                                                      Adamczewski M,
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414

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241 CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPOVSDAIPLLGTYFNCI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                        312 MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARV-
                                                                                                                                                                                        ----EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRL
                                                                                                                371 PPPPDLELRERSSKSLLANVLDIDDDFRH----PQAQQ-----PQCCRY---YRGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 17841; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.2%; Score 1417.5; DB 22;
87.2%; Pred. No. 2.2e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 17841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
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                                                                                                                                                                                                                                                                                          471 CLIIFTLFTIIATLAVLLSAPHIMV 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers
                                                                                                                                                                                                                                                                                                                                                                                                      ABB63683 standard; Protein; 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWD,
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 87.2%
Matches 265; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
N-PSDB; ABL07786.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DVDEKNQLLITUIMISLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 APAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                          Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 501;
                                                                                                                                                                                      acetyl-choline receptor protein from clone Hva7-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1803.5; DB 2
Pred. No. 8.2e-172;
3; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schulte T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1a; Page 22-23; 26pp; German
                                                                      AAY50816 standard; Protein; 501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant production of (II).
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68.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oellers N,
                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-014207/02.
N-PSDB; AAZ24477.
                                                                                                                                                                                                                                                                                  Heliothis virescens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adamczewski M,
                                                                                                                                                                                                                                                                                                                        DE19819829-A1.
                                                                                                                                                                                        H. virescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The alphal subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid sequences of chick neuronal alpha-bungarotcoxin binding protein (AABPP) were deduced from newly isolated DNR anlecules (AAT59196-97) obtd. from an 18-day chick embryo cDNR library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used
                                                   SFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVL
                                                                           MYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTY
                                                                                    LYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV
       GGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQL
                                                                                                            DGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                        Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic; ligand binding; ion channel.
                                                                                                                                                                                                                                                                                         Neuronal alpha-bungarotoxin binding protein alphal subunit.
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                                                                                                                                                                                                                                                                                                                                                                          23..502
/label= Mat_protein
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                                                                                                                                                                                                                                        AAW12368 standard; Protein; 502 AA
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                                                                                                                                                                                                                                                                          (first entry)
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N-PSDB; AAT59196.
                                                                                                                                                                                             310
                                                                                                                                                                             PLLG 305
                                                                                                                                                                                       PLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E----DKVRPACQHKQRRCSLSSMEMNTVSGQQCSNGNMLYIGFRGLDGVHCTPTTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 PQCCRYYRGG--EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKF
                                                                                                                                                                                                                                                    Gaps
in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intac ABBP subtypes. The ABBP alphal and alpha2 subunits can also be used to produce subunit peptides for use as immunogens for preparing antibodies to permit affinity purification of subtypes and their histological location.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                         Length 502;
                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 SATTPPPARVPPPDLELRERSSKSLLANVLD------
                                                                                                                                                                                                     47.5%; Score 1267; DB 18;
48.6%; Pred. No. 5.6e:118;
iive 83; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
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249; Conservative
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us-09-303-232-4.rag

Human, neuronal nicotinic acetylcholine receptor; alpha-7 subunit; brain tissue; screening; NAChR; antibody.

Location/Qualifiers

Homo sapiens,

Key Peptide Domain

Domain

1..23 /label= signal

Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.

(first entry)

14-MAY-1998

AAW44153;

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is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ATSDAVPLLGTYFLNMVAETMP-----ATSDAVPLLGTYFNCIM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FWVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP- 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 CRRVHADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQCRAES-----TYFNCIM
                                                                                                                                                                                                                                                                                                                                                                                         LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGFDSTYPTNVVVRNNGSCLYVPPG1FKSTCK1D1TWFPFDDORCEMKFGSWTYDGYOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALLGFTLPPDSGEKLSLGV----
                                                                                                                                                                                                                                                                                                                                              SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDR 469
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                                                                                                                                                                                                                                                                                                                           Indels 102;
                                                                                                                                                                                                                                                                                                    47.0%; Score 1253; DB 22; Length 498; llarity 50.4%; Pred. No. 1.4e-116; Conservative 53; Mismatches 108; Indels 102
                                                                                                                           Disclosure; SEQ ID NO 8088; 21pp + Sequence Listing; English.
                               Myers EW;
                              Li PWD,
                              Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                             al Similarity
267; Conserva
                                                  WPI; 2001-656860/75.
         (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                498 AA;
                                                              N-PSDB; ABL04535
                                                                                                         interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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46.0%; Pred. No. 7.2e-116;
iive 86; Mismatches 126;
/label
229..256
/label= TMD1
'~re= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                     /label= TMD4
/note= "transmembrane domain"
                                                                                                                                                                /note= "transmembrane domain"
                                                                                                                                                                                                                                                     /note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= cytoplasmic_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 80-81; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elliott KJ, Ellis SB, Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that express a variety of subtypes.
                                                                                                                                                                                                                                                                                                                  /note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SALK ) SALK INST BIOTECHNOLOGY (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                          /label= TMD3
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Matches 240; Conservative
                                                                                                                                                                                           290..317
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                                                                                                                                                                                                                                                                                                                                             462..487
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N-PSDB; AAV12197.
                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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AAW44153 standard; Protein; 502 AA.

AAW44153 ID AAW4 XX RESULT

9

Gaps

70;

183

251 240

123 191

131 63

300

392

452

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CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 APAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                          4 SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM
                                                                                                                                                                                                                                                                    DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                                                                                                                                                                                                          STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                                                                                                                                                                                                DEGGGDISSFVTNGEWELIGVPCKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive;
The alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAT48239). Host recombinant alpha-7 subunit, opt. in combination with other recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunits (see also AAW09018-24, AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                       Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG--
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                       ; Score 1246; DB 18;
; Pred. No. 7.2e-116;
86; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO2145 protein sequence SEQ ID NO:77
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Best Local Similarity 46.0%;
Matches 240; Conservative 86
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                                                                                                                                             DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                             STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                    APAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII
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                                                                                                                                                                                                                                           CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nicotinic acetylcholine receptor; nAChR; neurotransmitter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
                                                                                                                                                                                                                                                                                               312 MFMVASSVVSTILILLNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW09025 standard; Protein; 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0484722
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                      CVLIASMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
                                                                                                                                                                                                                                                                                                                                     -----SATTPPPAR-----SATTPPPAR
                                                                                                                                                                                                                                                          361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                          393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                  312 MFMVASSVVSTILLILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "conserved ligand-binding region, residues
Tyr210, Cys212, Cys213 and Tyr217 are
essential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; drug design; protein co-ordinate data; schizophrenia; Alzheimer's disease; nicotine addiction; Tourette's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108...115
/note= "conserved ligand-binding region,
Trp108 and Tyrl15 are essential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "conserved ligand-binding region,
                                                                                                                                                                                                                                                                                                                                                                                                                            SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                     453 DADISRDWKFAAMVVDRLCLIFFTEFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trp171 and Tyr173 are essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotinic acetylcholine receptor alpha7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; nootropic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200158951-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 APAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHOOMENTALAASLEHVSLOGEFORKLYKELVKNYNPLERPVANDSOPLTYYFSLSELOIM
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                                                                                                                                                                                                                                                                                                                                                                                                        Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.8%; Score 1246; DB 21; Length 502;
46.0%; Pred. No. 7.2e-116;
Live 86; Mismatches 126; Indels 70
                                                                                                                                                                                                                                                                                                                                                                                                        Gurney AL, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention describes an isolated antibody
                                                                                                                                                                                                                                                                                                                                                                                                        Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 61; Fig 58; 286pp; English.
                                                                                                                                                            99WO-US12252.
99US-0141037.
99US-0143048.
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99WO-US28313.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Wood WI;
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                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
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N-PSDB; AAC58395.
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WO200053755-A2
                                                                                                                                                                                                                                                                                                                                                                                                   Ashkenazi AJ,
                                                                                         06-JAN-2000;
                                                                                                                                                                                                                               26-JUL-1999;
30-NOV-1999;
20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe CK,
                                                                                                                                      08-MAR-1999
                                                                                                                                                              02-JUN-1999
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07-JUL-1999
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regions that are conserved throughout the various nach and which are essential for ligand binding. The invention relates to water soluble ligand-binding proteins derived from molluses, especially acetylcholine-binding proteins derived from molluses, especially acetylcholine-binding proteins derived from molluses, especially acetylcholine-binding proteins (AchBes) and analogues of ligand-gated ion channels, their crystals, and their water solubbe ligand of ligand-gated ion channels. The multimers and are amenable to crystallization. The crystal multimers and are amenable to crystallization. The crystal multimers and are amenable to crystallization. The crystal structure of AchBe is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and thus for screening of drugs that are capable of con channels. Chimeric proteins are provided that are capable of binding a ligand of a ligand-gated receptor, and comprise at least the anino acids of the AchBe determining solubility of the capable in the same positions as in the AchBe, and also comprising amino acids determining binding to the ligand. In the chimeric proteins, at least the essential amino acids of at least lof the conserved regions of an nAChR have been substituted for the conserved regions of an nAChR have been substituted for the
                                                                                                                                                                                            The sequence includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corresponding amino acids, and preferably entire stretches have been substituted. New drugs can be developed that selectively intervene in neuronal signalling pathways, especially where the ligand-gated ion channel is the nAchR, and the related disorder Tourette's syndrome, Alzheimer's disease, addiction to nicotine
                                                                                                                             is that of the alpha subunit of human
                                                                                                                                                                                      nicotinic acetylcholine receptor (nAChR).
Page 252-254; 260pp; English.
                                                                                                                             present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or schizophrenia
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502 AA; Sequence

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                                                                  APAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                      DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                                                                                            DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                                           : ||| :: |||||:||:||||| ||:|| E---ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTWRRRTLYYGLNLLIP
                                                                                                                                                                                                                                                              CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
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                                                                                                                                                                                                                                                                                                                                                                                               361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH---
                                                                                                                                                         STYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                                                                                                                                                   IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                             Gaps
                          70;
  Length 502;
                                                                                                                                                                                                                                                                                                                   312 MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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46.8%; Score 1246; DB 22;
46.0%; Pred. No. 7.2e-116;
tive 86; Mismatches 126;
             Local Similarity 46.0
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The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see ARC90382 and AB55014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVDEKNQLLITUIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH
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E---ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVDEKNOVLTTNIWLOMSWTDHYLOWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                             Human; alpha7 nicotinic acetylcholine gated ion char
5-hydroxytryptamine; 5-HT3; calcium ion conductance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.8%; Score 1246; DB 22;
46.0%; Pred. No. 7.2e-116;
tive 86; Mismatches 126;
                                                                                                                                             Wild-type human alpha7 ligand gated ion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Pages 61-63; 77pp; English.
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  AA.
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AAB50012 standard; Protein;
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                                                                                                (first entry)
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Best Local Similarity 46.0°
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Groppi VE, Wolfe ML,
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                                                                                                                                                                                                                                                                                                                    WO200073431-A2.
                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                             14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2000
                                                AAB50012;
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CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
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DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
                STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                        DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                               -----SATTPPPAR----SATTPPPAR-
                                                                                                                                                                                                                                                                                                                    361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                 393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                               312 MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nicotinic acetylcholine receptor; nNAChR; receptor; 7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                          453 DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                         SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 101; Column 59-64; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG70492 standard; Protein; 502 AA.
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92US-0938154
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93US-0149503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-711528/77.
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08-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare substantially free of contamination from amny other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha? subunit.
             392
                                                                                      Human; neuronal; nicotinic acetylcholine receptor; NAChR; drug screening;
immunochemistry; NAChR alpha7 subunit; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 APAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
             -- VPPPPDLELRERSSKSLLANVLD
                                       361 ORRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                  IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell comprising nucleic acids encoding human alpha and beta subunits neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                            453 DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                            SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.8%; Score 1246; DB 23;
46.0%; Pred. No. 7.2e-116;
Live 86; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chavez-Noriega LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examples; Page 130-131; 143pp; English.
                                                                                                                                                                                                                                                                                                                    Human neuronal NAChR alpha7 subunit.
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                                                                                                                                                                                                                              ABB82435 standard; Protein; 502
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Monteggia

McKenna DG,

Gopalakrishnan M,

(ABBO) ABBOTT

96US-0771737

22-DEC-1997; 20-DEC-1996;

02-JUL-1998

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Touma

Sullivan JP,

Briggs CA, Roch J, S

WPI; 1998-377593/32 N-PSDB; AAV44687.

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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR
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                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG---
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                                                                                                                                                                                                       6; DB 23;
7.2e-116;
                                                                                                                                                                                                                                     Mismatches 126;
                                                                                                                                                                                                       46.8%; Score 1246;
46.0%; Pred. No. 7.
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                                                                                                                                                                                                                                     86;
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This sequence is the V247T variant of human alpha7 nicotinic
acetylcholine receptor (nAChR) subunit of the invention. Cells containing
the DNB are used to express the protein and to identify modulators of
the DNB are used to express the protein and to identify modulators of
the DNB are used to express the protein and to identify modulators of
the DNB are used to express the protein and to identify modulators of
compounds or antagonists that are potentially useful for treating
neurodegeneration, enzyme dysfunction, affective disorders and immune
of systunction, such as cancer, post-herpetic neuralla, diabetic
neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
psychosis and schizophrenia. Probes based on the DNA are used to detect
the DNA in usual hybridisation or amplification tests, while monoclonal
antibodies are used to detect the protein for diagnosis (in vitro or by
in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
the protein has about 100-fold greater sensitivity. to cholinergic
receptor agonists (nicotine or acetylcholine) and response to these
agonists decays more slowly, but the wild-type inward rectification is
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                                                                                                                                                                                                                                                               Nucleic acid encoding variant of human alpha? nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the receptor, potentially useful for treating neuro-degeneration, cancer, affective disorders etc.
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45.8%; Pred. No. 1.8e-115;
tive 86; Mismatches 127;
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DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
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5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
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                                                                     453 DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                   46.5%; Score 1240; DB 22;
45.8%; Pred. No. 2.9e-115;
tive 86; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                            Mutant human alpha7 ligand gated ion channel #1.
                     ------GGOPPEG-
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230
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Best Local Similarity 45.83
Matches 239; Conservative
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Search completed: August 13, 2003, 15:25:26 Job time : 44.5088 secs

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RESULT 1
BG632919/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AL530299 AL530299
AK053497 Mus muscu
AK051730 Mus muscu
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11127.831 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                          22781392 seqs, 12152238056 residues
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                                                                                                                               US-09-303-232-3_COPY_335_1822
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                                                   nucleic search, using sw model
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AL530299
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Gapop 10.0 , Gapext 1.0
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Listing first 45 s
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AK081254 Mus muscu
CB149460 K EST0205
BX401124 BX403124
BU915857 AGENCOURT
BI516843 BB160023A
BI516843 BB160023A
AL058211 Drosophil
AL058211 Drosophil
AL073676 Drosophil
AL064281 Drosophil
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CA373069 647093 NC
AKO80415 Mus muscu
AKO29177 Mus muscu
AI292581 GH15518.5
AKO80475 Mus muscu
AKO49722 Mus muscu
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AU120692 AU120692
BW11715 UI-E-CLI-
BU702422 UI-M-FIO-
BU161024 AGENCOURT
BX421718 BX421718
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BQ720344 AGENCOURT
CA374163 648474 NC
BX299163 BX299163
AK041217 Mus muscu
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BI195149 602944157
AL210044 Tetraodon
AK030464 Mus muscu
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                                                               AK051742 Mus muscu
AK034228 Mus muscu
AK083157 Mus muscu
                                                                                         AK083157 Mus muscu
BU149265 AGENCOURT
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BE664308 148713 MA
AL192274 Tetraodon
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Drosophila melanogaster
Brusryota: Metazota, Arthropoda; Hazapoda; Insecta; Pterygota;
Neptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ hases 1 to 885)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.
BROPF/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                    BU149265
AK081254
CB149460
BX403124
BU915857
BU915857
BU516433
CB245337
CB24439
CNS0001F
CNS0001F
CNS0001C
                                                                                                                                                                                                                                                                     CA373069
AW013068
AW0120692
AW120692
BW11015
BW110102422
BW161024
BW487554
BW29163
AK041217
CA374163
CA326954
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CA3762B
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AK010496
BE664308
CNS02DCP
                                      AK080475
AK049722
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Contact: Stapleton, M.
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586
3827
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1101
1007
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720
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253.8
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241.4
235.8
2232.8
225.2
225.2
214.6
2114.6
2113.8
2113.8
203.8
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181.8
178.2
177.8
175.8
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172.6
172.6
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187.4
                                                                                                                                                                                                                                                                      202
199.6
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Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Sax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or

BDGP

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913
                                                                                                                                            DEFINITION
                                                                                                                                                                                                                ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIGITCCICAACAIGGIGGCGGAGACGAIGCCAGCGACGICGGACGCCGIGCCCIIGCIC 912
 was
         polyadenylated. The resulting Poly.T sequence has been removed. genomic AE003511: arm:X [18792641,19136447] estimated-cyto:18A3-18C6: 04/10/2001 Plate: GH.161 row: C column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTTCAATCTGATCGTGCCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACC
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                                                                                                                                                                                                                                                                                                          705 AGTGCCGACGAGGGCTTCGATGGAACGTACGCCACAAATGTGGTGGTTCGCAATAATGGG
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                                                                                                                                                                                                                                                                                                                                         253 TGGCTAAAACTAGAGTGGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGG
                                                                                                                                                                                                                                                                        Gaps
this clone
                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                Length 885;
more T residues at the beginning of the sequence,
                                                                                                                                                                                                                                                                       Indels
                                                                                   /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                Score 476.2; DB 10;
Pred. No. 9.6e-110;
0; Mismatches 223;
                                                     High quality sequence stop: 784. Location/Qualifiers
                                                                                                                       /clone="GH16126"
                                                                                                                                                                                                                                                32.0%;
illarity 73.2%;
Conservative
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                                                GGAACTTATTTCAATTGCATTATGTTATGGTGGCCTCATCAGTTGTGTCAACCATACTT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Concurrence received with the control of Sequence of Indivision of Invitrogen. This sequence belongs to sequence cluster of Meds. For more information about this cluster, see http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CSODD007CH03Qplscluster=7646.r. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD007CH03Qpl.
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
primer of the primer and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
326 c 319 g 273 t 25 others
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                               GTCCTCAATTATCATCATCATCATAGAAATCCAGATACGCATGAAATGAGTGAATGGGT
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Pred. No. 3e-70;
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="CS0DD007YP05
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il Similarity 60.0%;
564; Conservative
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Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Bunchelloral annowation of a fill langth mouse on a man Hayashizaki,Y.
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Analysis of the mouse transcriptome based on functional annotation of 60/700 full-length cDNAs

Lature 420, 563-573 (2002)

6 (bases 1 to 1864)

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Direct Submission
Submitted (16-701-2001) Yoshinlade Hayashizaki, The Institute of Submitted (16-701-2001) Yoshinlade Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research
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prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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Nature 409 (6821), 685-690 (2001)
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Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:El30103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  548
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                               CATCTGGCTAAAACTAGAGTGGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGG
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                                                                                            CGGGGTCAAAGATTTAAGAGTGCCACCCCACAGACTATGGAAACCAGACGTCCTTATGTA
                                                                                                                                                                                                                                                                                                             907 TIGCICGCCACCTACTICAACTGCATCATGTICATGGTGG 946
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Meth. Enzymol. 303, 19-44 (1999)
99279253
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628 703 688 763 748 823 808 883 868 943 928

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Mus musculus 12 days embryo spinal ganglion cDNA, RIKBN full-length enriched library, clone:D130068A06 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence. AKO51730.1 GI:26342155 HTC; CAP trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                             TCA---TTGGCTCCTCCATGAACCTCAAGGACTATTGGGAAAGTGGCGAGTGGGCCATCA
                                                                                                                                                                                                                                                      GAGAAAAGTTGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGG
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                                                       AAAACTGCACCATGAAGTTCGGCTCCTGGTCCTACGACAAGGCAAAGATCGACCTGGTCC
                                                                                                                                                                                                  704 TTAAAGCCCCGGGCTACAAACATGAAATCAAGTACAACTGCTGTGAGGAGATCTACCAAG
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                                                                                          TACAGGATGAAGGGGGGGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAA
                                                                                                                                                                 TAGGAGTCCCCGGCAAGCGCAACGAGATCTACTACAACTGTTGTCCGGAGCCATACATCG
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/db_xref="G1:26543495"
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RPVANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLMLKQIWNDYKLKWKPSDYQGVEF
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PFDYQNCTWKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEIKYNCC
EEIYQDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYLPSDCGEKVTLCISVLLS
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WKARVELLDFWMFWTRPGYBEDAFTRNFYGAELSMLCFSRADSKSCKEGYPCO
DGTCGYCHRRPK ISNFSANITRSSSSESVDAVLSLSALSPEIKEA IQSVKYIAENMK
AQNYAKEIQDDWXYVAMVIDRIFLWYFILVCILGTAGIELQPLMARDDF"
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0; Mismatches 469;
                                                                                                                                       /db_xref="FANTOM_DB:E130103E14"
/db_xref="taxon:10090"
/clone="E130103E14"
                                                                                                                                                                                            /tissue_type="eyeball"
/clone_lib="RIKEN full-length
/dev_stage="0 day neonate"
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
                                                                                        /organism="Mus musculus"
                                                       Location/Qualifiers
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Analysis of the mouse transcriptome based on functional annotation of 60/70f full-length CDNAs

Nature 420, 563-573 (2002)

E (bases I to 2916)

S Adachi, J. Alzawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanaqaki, T., Haraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hortani, K., Ishii, Y., Itoh, M., Ragawa, I., Kasukawa, T., Katoh, H., Kawai, J., Koljma, Y., Mondo, S., Konno, H., Kouda, M., Kojama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Santo, R., Salto, R., Saltoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shiraki, T., Tanaka, T., Tanaka, T., Yasunishi, A., Kumata, M., Taqami, M., Taqawa, A., Taya, T., Yasunishi, A., Kumata, M., Manaka, M., Taqami, M., Toqaru, A., Toya, T., Yasunishi, A., Kumata, M., Manaka, M., Taqami, A., Toya, T., Yasunishi, A.,
                                Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishlkawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIEB, Integrated sequence analysis (RISA) system--384-format Sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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      Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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URL:http://fantom.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                     /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 GGAATGACTACAAGCTGAAATGGAAACCCTCTGACTACCAAGGGGTGGAGTTCATGCGAG
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_xref="FANTOM_DB:D130068A06"
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Pred. No. 3.4
                                                  /db_xref="taxon:10090"
/clone="D130068A06"
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arawawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashurner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Couackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission of the State of Submission of Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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/note="unnamed protein product; NEURONAL NICOTINIC
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152. .1666
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/clone="A730007P14"
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/strain="C57BL/6J"
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3126 bp mRNA linear HTC 05-DEC-2002
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:3473000/214 product:NEURONAL UCCTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
                                                                                                                                                                                                                                                                                                                                                                               1080 TCACTATGATTTTTGTCACCTTGTCCATCGTCATCACAGTCTTTGTGCTCAACGTGCACT 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    989 ACCGGCACGCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGC 1048
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                             929 GCATCATGTTCATGGTGGCTTCCTCCGTCGTCCTCACCATACTGATCCTCAACTACCACC
                                                                                                                                                                                                                                                                                            900 INCCGIGCTCATCTCCTTCCTCACTGTGCTCTTCTACCTGCCCTCCGACTGTG
                                                                                                                                                                                                                                                                                                                                              809 GAGAAAAGTIGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .020 TCACCGAGACCATCCTTCCACCTCACTGGTCATCCCTTGATCGGGGAGTACCTCCTT
                        TAGGAGTCCCCGGCAAGCGCAACGAGATCTACAAACTGTTGTCCGGAGCCATACATCG
                                                                             780 TTAAAGCCCCGGGCTACAAACATGAAATCAAGTACAACTGCTGTGAGGAGATCTACCAAG
                                                                                                                                  ACATCACGTTTGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCG
                                                                                                                                                                                                                                        749 TGCCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Weth-Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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HTMPTWYKAVFLNLLPRVMFTRPTSTBEDAPKTRFYGAELSNLNCFSRADSKSCKE
GYPCODGTCGYCHHREYKISHFSANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYI
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                                                               /protein_id="BaC37909.1"
/db_xref="G1:26548539"
/tb_xref="G1:26548539"
/translation="mrsSDMGVVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFED YNEINEVANVSHPYNIQFEVSMSQLVKVDEVNQIMETNLMLKQIWNDYKLKWRPSDY GGVEFWRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKI DVTYFPFDYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEI
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ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497) putative"
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Ltoh, M., Konno, H., Okazaki, Y., Muramatsu, M., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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  TGCCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCG
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Mus musculus 0 day neonate head cDNA, RIKEN full-length library, clone:4831406G09 product:cholinergic receptor, alpha polypeptide 1 (muscle), full insert sequence.

AKU29177
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High efficiency full-length CDNA
Meth. Enzymol. 303, 19-44 (1999)
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NCSWKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKEARGWKHWVFYSCCPTTPY
LDITYHFVWQRLPLYFIVNVIIPCLLFSFLTSLVFYLPTDSGEKMTLSISVLLSLTVF
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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/tissue="4831406G09"
/tissue_type="10ed"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4290)
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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Nature 409 (6821), 685-690 (2001)
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Please visit our web site for further details.
Please visit our web site for jp/.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                          112 AAGCTGTCAAGGACCTCATGAAAAGCGCCTGCTGAACCATCTGCTGTGCCACCTACAATAC
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enriched library, clone:A730038F14 product:NEURONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                    141 ACTGGAGAGCCCGTCGTCAACGAGAGCGACCCGCTGCAGCTCTCCTTCGGCCTCACGCT
                                                                                                          GCTGGAGCGACCCGTGGCCAATGAATCGGAGCCCTGGAGGTTAAGTTCGGACTGACGT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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G07 bp mRNA linear EST 23-APR-2001
G15518.5518.5prime GH Drosophila melanogaster head poT2 Drosophila
melanogaster cDNA clone GH15518 5 similar to CG4128: FBan0004128
'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence.
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/dev_stage="adult"
/dat_bost="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
//Apol; Sized fractionated cDNAs were directly ligated into
                                                                                                     915 CACCTACTICAACTGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTGAT 974
                                                                                                                              845 GITCCIICIGGICAITGIGGAGCIAAICCCIICCACCICCAGGGCIGIGCCCCIGAICGG 904
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I (bases I to 607)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
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                      GTTCCTCAACATGGTGGCGGAGACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003626; arm:2L [9617316,9882551]
estlimated-cyto:30C7-30F4: 04/10/2001
Plate: GH.155 row: B column: 6
High quality sequence stop: 521
POLYA=No.
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    .607
    /organism="Drosophila melanogaster"
/mol_type="mRNA"
    /db_xref="taxon:7227"

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Pred. No. 2.1e-57;
0; Mismatches 171;
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Other_ESTs: GH15518.3prime
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68.5%;
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/db_xref="taxon:10090"
/clone="taxon:10090"
/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2010)
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Nature 409 (6821), 685-690 (2001)
sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/mol_type="mRNA"
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/dev_stage="7 days neonate"
167. .1673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               720 CCTC --- ATTGGCTCCTCCATGAACCTCAAGGACTATTGGGAAAGTGGCGAGTGGGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 GGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 TGCCACCCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGGGGGGGACGAAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 TCCCTGCAGAGAAGATCTGGAAACCAGACATCGTGCTTTACAACAACGCCGATGGGGGATT
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                                                                                                                                                                                                                                                             29 TGGCGCCCCCCCCCGCGGCCTGCTGCTGCTGTGCCTCTCGCCCGAGGGGGGCCCACGCT
                                                                                                                                                                                                                                                                                                  180 TGCCCCCCCCCCCCCTGTCCATGCTGATGCTGGTGCTGATGCTGCTGCTGCCAGTGGCCAGCG
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                                                     SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%Length, match=1497) putative." 465 g 520 t
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                                                                                                                                                                                                                       Indels
                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                     0; Mismatches 461;
                                                                                                                                                                              Score 263.4; DB 1
Pred, No. 1.2e-55;
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L. Nature 420, 563-573 (2002)

E. (bases 1 to 4037)

S. Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatawa, T., Katoh, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kayai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakanura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazuki, Y., Saki, Saki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Towara, T., Yasunishi, A., Tayanishi, T., Waranishi, A., Towaranishi, T., Tayanishi, A., Toya, T., Yasunishi, A., Toya, T., Yasunishi, A.,
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HFPFDQQNCTMKFRSWTYDRTEIDLVLKSDVASLDDFTPSGEWDIIALPGRRNENPDD
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TVEVLLISKYVPPTSLDVPLVGKYLMETWOLVTRSIVTSVCVLNVHHRSPTHTWAPW
VYKVELEKLPPLLFLQOPRHFCARQRIKLRRRQREBGAGTLEFREGPAADPCTCFVN
PASWOGLAGAFOAEDAAGLGSNGPCSCGIREAVDGVRFIADHWRSEDDDOSVREDW
KYVAMVĮDRLFLMIFVFVCVFGIIGMFLQPLFQNYTATTFLHSDHSAPSSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
200. .1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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//note="unnamed protein product; cholinergic receptor,
nicotinic, beta polypeptide 2 (neuronal) (WGD)MGI:87891,
GB|NM_009602, evidence: BLASTN, 99%, match=1498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                             The FANTOM Consortium and the RIKEN Genome Exploration Research
annotation of a full-length mouse cDNA collection (6821), 685-690 (2001)
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Please visit our web site for further details.
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Pred. No. 3.7e-54;
0; Mismatches 640;
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Best Local Similarity 51.5%;
Matches 709; Conservative
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                                        JOURNAL
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Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530044Pi6 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                    987 CCACCGGCACGCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTG 1046
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
      927 CIGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTGATCCTCAACTACCA
                                                                   1077 CITCACIATGAITITIGICACCITGICCAICGICAICACAGICITIGIGCICAACGIGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK049722.1 GI:26340459
HTC; CAP trapper.
                                                                                                                                                                                                                                                                 1047 GCTGCCGTGGG 1057
                                                                                                                                                                                                                                                                                                                                  1197 TCTCCCCCAGG 1207
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	ACCACGAGAAGCGGCTACTGCACCACCTATTGGA	ACACAGAGGAGCGGCTGGTGGAGCATCTTTGGATCCTTCCGGCTATAACAAGCTGATCC	GGCCCGTCGTCAACGAGGGACCCGCTGCAGCTCTCCGTTCGGCCTCACGCTCATGCAGA		TCATCGACGTGGACGAGAAGCAGCTTTTAATAACAAACATCTGGCTAAAACTAGAGT		GGAATGATGATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAG		TGCCACCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGGGGGGGAGGAAGGGT	99	TCGACAGCACGTATCCAACGAACGTGGTGGTGCGGAACACGGCTCGTGTCTGTACGTGC	ACGAAGTCTCTTCTATTCCAATGCTGTGGTCCTCTATGATGGCAGCATCTTTGGCTAC	CGCCCGGCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACC	CGCCTGCCATCTACAAGAGGGCATGCAAGATTGAGGTGAAGCACTTCCCATTTGACCAGC	AACGATGCGAGATGAGATTTGCAGCTGGACTTATGATGGTTGCGTTTGGATTTACAAC 			1 # C & E C E	INSTRUCTOR OF THE PROPERTY OF	ACATCACGTTTGCGGTGGTGGTGGTGGTGGAAAACGCTCTACTACTTCTAATCG	ACATCACCACGACTTCATCATTCGTCGCAAACCGCTCTTCTACACCATCAACCTCATCA	TGCCCTGCGTGCTCATCGCCTCCATGGGGTTCACCTTGCCTCCAGACTCCG	TCCCCTGCGTACTCATCACCTCGCTGGCCATCCTGGTCTTCTACCTGCCCTCAGACTGTG	GAGAAAAGTIGICTITAGGIGIGACGATATIACIGICGIIGACGGIGIICCICAACAIGG	GIGAAAAGAIGACACITIGIAITICIGIGCIGCIGGCGCICACGGIGITCCIGCIGCICA	TGGCGGAGACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTACTTCAACT	GCATCATGTTCATGTTGGCTTCCTCCTCCTCCCCCCCCCC	TCACCATGGTGCTAGTCACCTTCTCCATCGTCACTAGCGTGTGTGT	ACCGGCACGCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGCTTCTTTATTGCC		TGCCGTGGGTGCTGCGCATGTCACGGCCCGGCTCGGCGACGACGCCGCCGCCGCGCGCG	TGCCCACCCTCTTCCTGCAGCAGCACGCCACGCTGTGCACGTCAACGCCTGCGCT	TACCTCCGCCGCGGACCTGGAGCTGCGCGCGGGCGCTCCTCCAAGTCGCTCCTAGCGAACG	TGCGAAGGCGCCAGCGGAACGTGAGGGGGCAGGCACACTATTCTTCCGCGAAGGTCCTG
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	TACTGC.	rggrgg,	AGAGCG	 SCTCTG	AGAAGA	AGCGGG	TGAGGT	 CACAT	TATGGA	 rcreec	CAACGAA	ATTCCA	AGAGCA	AGAGCG	ATGAAGTTTG		GCAG	40000	BACGCA	TGGTGA	TCATCA	rcccr	rcaccr	TAGGTG	TTTGTA	CAGCGA	1123371	TCACCT	CTCACG	CGCACA	GCATGT	TCCTGC	ACCTGG	GGGAAC
	AGCGGC	AGCGGC	TCAACG	 CTAATG	TGGACG	II IIIII TGCACGAG	TGAACT	ATCGCC	ACAGAC	 AGCACA	CGTATO	CCTICI	TCTTCA	TCTACA	AGATGA -		ATGTGG	***************************************	CAGGCC	TTGCGG	ACGACT	TGCTCA	TACTCA	TGTCTT	rgacac	CGATGC	TCATGG	I I	CAGACA	CTACCA	TGCTGC	TCCTCT	990090	GCCAGC
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us musculus 12 days embryo spinal ganglion cDNA, RikEn full-length incitched library, clone:D130070121 product:Cholinergic receptor, toctinic, beta polypeptide 2 (neuronal), full insert sequence. (051742. G1:26342173
                                                                               CAGCTGACCCATGTACCTGCTTTGTCAATCCTGCATGAATGCAGGGCTTGGCTGGGGCTT 1406
                                                                                                                                                                                                                                                                                                                            ACTACGAGCTCTCCCTCATTCTGAAGGAGATTAGAGTCATCACAGATCAGATGCGCAAGG 1348
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                                                                                                                                                                                                           ------CTCCGGGAAGCTGTGGACGGTGTACGCTTCATTGCGGACCATATGCGAAGTG 1517
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mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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gh-efficiency full-length cDNA cloning
th. Enzymol. 303, 19-44 (1999)
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Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Sting, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., and Hayashizaki, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (16-JUU-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, TRE.), Tel:81-45-503-9222, Fax:81-45-503-9216)
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/db_xref="FANTOM_DB:D130070121"
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/clone_lb="RIKEN full-length enriched mouse cDNA library"
/dev_staip="12 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachl, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, K., Hirzanca, T., Hirzanca, T., Hirzanca, T., Hirzanca, T., Hirzanca, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Miyazaki, A., Murzata, M., Nakamura, M., Nishi, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takaku-Akahira, S., Murantsu, M., and Hayashizaki, Y., Tasunishi, A., Takaku-Akahira, S., Murantsu, M., and Hayashizaki, Y., Tayay, T., Yasunishi, A.,
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HFPFDQQNCTMKFRSWTYDRTEIDLVLKSDVASLLDBFTPSGEWDIIALPGRRNENPDD
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TVFLLLISKIVPPTSLDVPLVGKYLMFTMVLVTFSIVTSVCVLNVHHRSPTTHTMAPW
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

( Passars I to 4046)

Adachi, J. Alazawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product; cholinergic receptor,
nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASTN, 99%, match=1498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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KYVAMVIDRLFLWIFVFVCVFGTIGMFLQPLFQNYTATTFLHSDHSAPSSK"
1 1127 c 1077 g 964 t
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                                                                                                                                                                                                                   348 GTCCAGCTACTAATGGCTCTGAGCTGACTGTACAGCTCATGGTATCATTGGCACAGC
                                                                                                                                                                                                                                                 GGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAG
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                                                                       Score 258; DB 11;
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Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gasterland,T., Gissi,C., King,B., Kochiwa,H., Fleischmann,W.; Sarai,K., Matsudo,I., King,B., Kochiwa,H., Kueh,P., Lewis,S., Matsuo,Y., Nikalido,I., Rozuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuo,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bolinga,N., Carninci,P., de Bonaldo,M.F., Brownstehn,M.J., But,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Nordone,P., Ring,B., Kingwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A. Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y. Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adachl, J. Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozame, T., Hayashida, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kaukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nakamura, M., Nakamura, M., Nakamura, M., Saito, R., Saitoh, H., Sakai, K., Saito, R., Saito, R., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Physical and Chemical Research (RIKEM), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 565-573 (2002)
6 (bases 1 to 2940)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome conscious description of Experimental Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
      Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product; cholinergic recepnication; alpha polypeptide 4 (MGD|MG1:87888, GB|NM_015730, evidence: BLASTN, 99%, match=1946)
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/db_xref="taxon:10090"
/clone="9330165116"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/organism="Mus musculus"
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone: 630019M18 product: cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.
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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new g.
20499374
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                                                                                                                 ATCCCGTCCACCTCGCTGGTCATCCCGCTCATCGGCGAGTACCTGCTCTTCACCATGATC
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ATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTACTTCAACTGCATCTTC
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High-efficiency full-length cDNA cloning
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TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLAMFIIVCLLGTVGLFLPPW
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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L (bases I to 3230)

S Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Haramoto,K., Hirooka,T., Hirozane,T.,
Rukuda,S., Furuno,M., Hanagaki,T., Hara,K., M., Kagawa,I., Kasukawa,T.,
Ratoh,H., Kawal,J., Kohjina,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kutihara,C., Matsuyama,T., Myazaki,A., Marata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Salto,R., Saltoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Saltoh,R., Shinagawa,A., Shiraki,T.,
Sand,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Muramatsu,M. and Hayashizaki,Y.,
Direct Submission
Submitted (16-Par-202) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
KIREN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-resegoscriken.go.jp,
NEL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSPRTHTMPAMVRRVFLDIVPRLLFMKRPSVVKDNCRRLIESMHKMANAPRFWPEPES
EPGILGDICNOGLSPAPTFCNRMDTAVETQPTCRSPSHKVPDLKTSEVEKASPCPSPG
SCHPPNSSGAPVLIKARSLSVQHVPSSQEAAEGSIRCRSRSIQYCVSQDGAASLTESK
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RLFSGYNKWSRPVANISDVVLVRFGLSIAQLIDVDEKNOMMTTUVWVKQEWHDYKLRW
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TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSECGEK
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       Suzuki, H.,
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Punctional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unnamed protein product; cholinergic receptor.
nicotinic, alpha polypeptide 4 (MGD|MGI:87888,
GB|NM_015730, evidence: BLASTN, 99%, match=1946)
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Please visit our web site for further details
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="hippocampus"
/clone_lib="RIKEN full-length
/dev_stage="adult"
36. .1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/db_xref="GI:26350297"
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/strain="C57BL/6J"
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Best Local S:
Matches 532,
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakayuchi,S., Ikeqami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MNNA linear HTC 05-DEC-2
MNS musculus adult male corpus striatum cDNA, RIKBN full.length
enriched library, clone: C03030P04 product: cholinergic receptor,
incotinic, beta polypeptide 2 (neuronal), full insert sequence.
                                                                                                                    335 CCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACA
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                                                                                     ATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCCAC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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Tissue Procurement: Dr. James R. Lupski
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Gases I to 3483

E (bases 1 to 3483)

E (bases 1 to 
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yokohama,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/.URL:http://fantom.gsc.riken.go.jp/.Location/Qualifiers
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/db_xref="taxon:10090"
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/mol_type="mRNA"
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/tissue_type="corpus striatum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev_stage="adult"
1. 3483
/note="cholinergic receptor, nicotinic, beta polypeptide 2
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                                                                                                                                                                                                                                                                                                                              3;
                                                                                                 (neuronal) (MGD[MGI:87891, GB|NM_009602, evidence: BLASTN, 99%, match=1498)"
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                                                                                                                                                                                                                                                                                                                                                                                                                     ACACAGAGGAGGGGCTGGTGGAGCATCTTGGATCCTTCCCGCTATAACAAGCTGATCC 342
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                                                                                                                                                                                                                                                                                                                              18; Gaps
                                                                                                                                                                                                                                                                             Score 244.4; DB 11; Length 3483;
Pred. No. 9.8e-51;
0; Mismatches 426; Indels 18;
/clone="C030030P04"
                                                                                                                                                                                                                                                                               tch 16.4%;
al Similarity 55.2%;
548; Conservative
                        /sex="male"
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ORIGIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 615) Kim, N. S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: Liver; Vector: pCNS-D2; Site_1: ECORI; Site_2: NOtI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECORI site by treatment of T4 RNA linker including strand cDNA was synthesized from oilgo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was acticularized with E. coll DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand
CB149460 615 bp mRNA linear EST 29-JAN-2003 K-EST0205995 L15CKK1 Homo sapiens cDNA clone L15CKK1-50-D08 5',
                                                                      obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  converted to a DNA strand by Okayama-Berg method. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                      1049 TGCCGTGGGTGCTGCGCATGTCACGGCCCGGC 1080
                                                                                                                                                                                        21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: yongsung@mail.kribb.re.kr
Plate: 50 row: D column: 08
High quality sequence stop: 615.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:9606"
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CB149460.1 GI:28132277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +82-42-860-4409
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atch 16.2%; cal Similarity 63.1%; 393; Conservative

Query Match Best Local

Matches

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Mutant human alpha Mutant human alpha Mutant human alpha V274T variant huma Human polynucleoti

Human neuronal nic Human PRO2145 nucl

Human neuronal NAC

Neuronal nicotinic Prostate cancer-as Drosophila melanog Neuronal nicotinic Chimeric alpha7/5-Human mutant neuro AnA encoding novel Alpha4 subunit of Human neuronal NAC

Alpha 2 subunit of Human neuronal NAC Human neuronal nic

Neuronal alpha-bun Neuronal alpha-bun Human neuronal nic

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Human neuronal nic

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                                                                                                                          This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insectivated. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Hellothus virescens.
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               2000-014207/02
                              P-PSDB; AAY50815
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                                                      CTCACACTTGGAGTCACTATTCTTTCTATCGCTGACGTGTTCCTCAACCTGGTAGCCGAG
                                                                                                                                                                                                                                                                ACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTACTTCAACTGCATCATG
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                                                                                                             GTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCGGAGAAAG
                                                                                                                                                                                      TTGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGGTGGCGGAG
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                                       TITGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCGTGCCCTGC
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                                                                                                                                                                                                                                                                                                             This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGTACTGGAGAGGCCCGTC 156
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Pred. No. 3.7e-130;
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Local Similarity 64.6%;
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                                                                     2182 TGATCCTAGAGTTCCCGACCACGCCCTGTTCGGACACAT-----CCTCCGAGCGGAAGCAC
                                                                                                                                   CAGATACTCTCCGACGTTGAGCTGAAAGAGCGCTCGTCGAAATCGCTGCTGGCCAACGTA
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                                                 CAGGATGAAGGGGGGGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAATA
                                                                                                                   GGAGTCCCCGGCAAGCGCAACGAGATCTACTACAACTGTTGTCCGGAGCCATACATCGAC
                                                                                                                                                                                       ATCACGTTTGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCGTG
                                                                                                                                                                                                                                                          CCCIGCGIGCICATCGCCICCATGGCICIATIGGGGITCACCITGCCICCAGACICCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, lits regulatory regions, and antibodies directed against (1) encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (1) are also used to recombinant production of (11). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGTACTGGAGAGG
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                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 512.8; DB 21; Length 2886; Pred. No. 5.4e-115;
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                                                                 "acetyl choline receptor.
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0; Mismatches 502;
                Location/Qualifiers
372..2684
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62.5%;
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P-PSDB; AAY50814.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
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                                                                                   CCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCGGA
                                 CCAGGTATATTTAAGTCAACGTGTAAGATCGACATTACGTGGTTTCCATTCGACGATCAG
                                                                                                                                                  GAAAAGTTGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGGTG
                                                                  CGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAACTA
                                                                                                                               CAGGATGAAGGGGGCGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAATA
                                                                                                                                                                                                 GGAGTCCCCGGCAAGCGCAACGAGATCTACTACAACTGTTGTCCGGAGCCATACATCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 16175; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide SEQ ID
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01616 ABL0051), expressed DNA sequences (ABL016176 ABL0511), expressed DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 35681
                                                              developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23; Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 936 BP; 238 A; 213 C; 239 G; 246 T; 0 other;
                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                               PWD,
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Best Local Similarity 72.9%;
Matches 605; Conservative
                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
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11-JUL-2000; 2000US-0614150
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                                                                              pharmaceutical; gene; ss
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P-PSDB; ABB69630.
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   1072 CTCGTCGGTGCTGCTGACAGTAGTGGTGCTCAACTACCACCATCGCACAGCGGACATTCA
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5-hydroxytryptamine; 5-HT3; calcium ion conductance;
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useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed
                                                                   specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                           Score 458.2; DB 23; Length 1540;
Pred. No. 9e-102;
0; Mismatches 493; Indels 99;
                                                                                                                    Sequence 1540 BP; 412 A; 390 C; 376 G; 362 T; 0 other;
                                                                                                                                          Match 30.8%;
Local Similarity 60.1%;
hes 893; Conservative
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Score 405.6; DB 22; Length 1509;
Pred. No. 6.1e-89;
0; Mismatches 604; Indels 42;
                                                                                                                 Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;
Example 5; Pages 60-61; 77pp; English
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al Similarity 56.5%;
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                                                                                                The present sequence is the coding sequence for wild-type human alpha7 national cacetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells.
                                                                                                                                                                                                                                                                                                    CGCCGGGAGGCGTCTGGCTGGCCGCTCGCTCCTGCACGTGTCCCTGCAAGGCG
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Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
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AGTTGTCTTTAGGTGTGGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGGTGGCGG
                                          AGACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTACTTCAACTGCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                           the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammallan cells or amphibian oocytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAY48232-38, AAY48240-41), express recombinant nAChR subunits useful for identifying cpds. that
                                                                                                                                                                   Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
                                                                                                                                                                                                                                              DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025)
                                                                                                                                                                                                                                                                                                                                                                                                 Score 405.6; DB 18; Length 1876;
Pred. No. 6.5e-89;
0; Mismatches 604; Indels 42;
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 other;
                                                                                                                                                                                                              Disclosure; Page 71-73; 108pp; English.
                                                                                                                                                                                                                                                                                                                                       modulate the activity of human nAChRs.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.3%;
Best Local Similarity 56.5%;
Matches 840; Conservative
                                                          (SIBI-) SIBIA NEUROSCIENCES
96WO-US09775
                              95US-0484722
                                                                                         Elliott KJ, Harpold MM;
                                                                                                                    WPI; 1997-065463/06.
P-PSDB; AAW09025.
07-JUN-1996;
                              07-JUN-1995;
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                                    443 CCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATTGCCAGTACCTGCCTCCAG
                                                                    GCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACCAACGAT
                                                                                     GCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAACTACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta MAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and design of individual subunits and should lead to the identification and design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 ATGGCCAGATTTGGAAACCAGACATTCTTCTCTATAACAGTGCTGATGAGGGCTTTGACG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compounds that are capable of very specific interaction with one or
more receptor subtypes. The resulting drugs should exhibit fewer
unwanted side effects than drugs identified e.g. screening with cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCCGGGAGGCGTCTGCCTGCCTGCCGCGTCGCTCCTGCACGTGTCCCTGCAAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGTGGACGAGAACCAGCTTTTAATAACAAACATCTGGCTAAAACTAGAATG
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                                                 "neuronal nicotinic acetylcholine receptor alpha-7 subunit"
                                                                                                                                                                                                                                                                                                                                                             Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 1876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 405.2; DB 15;
Pred. No. 8.2e-89;
1; Mismatches 604;
                                                                                                                                                                                                                               (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC. (SIBI-) SIBIA NEUROSCIENCES INC.
Location/Qualifiers
73..1581
/*tag= a
/product= "neuronal n
                                                                                                                                                                                                                                                                                 Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 78-79; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that express a variety of subtypes.
                                                                                                                                                                                                                                                SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 27.2%;
al Similarity 56.5%;
839; Conservative 1
                                                                                                                                                                 94WO-US02447
                                                                                                                                                                                                93US-0028031
                                                                                                                                                                                                                                                                                                                                                                                                 activity of the receptor
                                                                                                                                                                                                                                                                                 Ellis SB,
                                                                                                                                                                                                                                                                                                                WPI; 1994-303024/37.
                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW44153
                                                                                                  WO9420617-A2
                                                                                                                                                               08-MAR-1994;
                                                                                                                                                                                                08-MAR-1993;
                                                                                                                                                                                                                                                                               Elliott KJ,
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Best Local Si
Matches 839,
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623 A------GGCAGATATCAGTGGCTATATCCCCAATGGAGAATGGGACCTAGTGGGAA 673
                                             203 TGGCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCCTCCTGCAGATCATGG
                                                                                           183 ATGGCCAGATTTGGAAACCAGACATTCTCTATAACAGTGCTGATGAGCGCTTTGACG
                                                                                                                                                                                                                                                                                                                                                                                                   AGACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTACTTCAACTGCATCA
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                                                                                                                                                                                                   CCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACA
                                                                                                                                                                                                                                                              GCACGTATCCAACGAACGTGGTGCTGCTGCAACAACGCCTCGTGTCTGTACGTGCCCCCC
                                                                                                                                                                                                                                                                               GCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCGGAGAAA
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                 TCGTCAACGAGAGCGACCCGCTGCAGCTCTCCGCCTCACGCCTCATGCAGATCATCG
                                                                                                                                       275 ATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCCAC
                                                                                                                                                                                                                                                                                                                                       GCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAACTACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleorides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha? subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 CGCCGGGAGGCGTCTGGCTGGCGCTGGCGGTCGCTCTGCACGTGTCCCTGCAAGGCG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGTACTGGAGAGGCCCG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; neuronal; nicotinic acetylcholine receptor; NAChR; drug screening; immunochemistry; NAChR alpha7 subunit; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell comprising nucleic acids encoding human alpha and beta subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Elliott KJ;
                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "NAChR alpha7 subunit"
/note= "neuronal nicotinic acetylcholine receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1876;
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604; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                     neuronal NAChR alpha7 subunit encoding cDNA
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Pred. No. 8.2e-89;
1; Mismatches 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chavez-Noriega LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examples; Page 129-130; 143pp; English.
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73..1581
                                                                                           BP
                                                                                          ABV73248 standard; cDNA; 1876
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ilarity 56.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MERI ) MERCK & CO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-2001;
                                                                                                                                                                                                                                                               Homo sapiens
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               1514
                                                                                                                        ABV73248;
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CCTTCACAGTGACCATGCGCCGCAGGACGTCTACTATGCCCTCAACCTGCTGATCCCCT 793
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 nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human nNAChR polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                          335 CCCACAGAGTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 ACGTGGATGAGAACAACTTTTAACCACCAACATTTGGCTGCAAATGTCTTGGACAG
                                                                                                                                                                                                                                                                                                                                                                                        275 ATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 ATGGCCAGATTTGGAAACCAGACATTCTTCTCTATAACAGTGCTGATGAGCGCTTTGACG
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                                                                                                                                                                              CGCCGGGGAGGCGTCTGGCTGGCGCTGGCCGCGTCGCTCCTGCACGTGCCAAGGCG
                                                                                                                                                                                                           ACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGTACTGGAGAGCCCCG
                                                                                                                                                                                                                           TCGTCAACGAGGGGCCCGCTGCAGCTCTTCGGCCTCACGCTCATGCAGATCATCG
                                                                                                                                                                                                                                                                                                                             215 ACGTGGACGAGAAGAACCAGCTTTTAATAACAAACATCTGGCTAAAAACTAGAGTGGAATG
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                                                                                       DB 24; Length 1876;
                                                                                                                  1; Mismatches 604; Indels
                                                          Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;
                                                                                      Score 405.2; DB 2
Pred. No. 8.2e-89;
                                                                                      27.2%;
56.5%;
                                                                                                                  839; Conservative
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                                                                                                                                    1226 GATACTACAGGGGGGGGGGAGAATGGCGCGGGGTTGGCGGCGCGCACAGTTGCTTCGGTG 1285
                                                                              TGCACGGGGGCCAACCCCCGGAGGGGGACCCGGACTTGGCCAAGATCCTGGAGGAGGTCC 1393
                                                                                                                                                                           AGTICGCCGCCAIGGTCGTGGACAGACTGTGCCTTATTATCTTTACCCTGTTCACAATCA 1441
                                                                                                                  GAGTCATCACAGATCAGATGCGCAAGGACGACGAAGATGCGGACATTTCGCGCGACTGGA 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for identifying compounds that are matagonists or agonists of human neuronal nicotinic acctylcholine receptors (nNAChRs). By contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an
                                                            -----ATTCTGAAGGAGATTA
                           Human neuronal nicotinic acetylcholine receptor alpha 7 subunit cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; neuronal nicotinic acetylcholine receptor; nNAChR; gene; ton flux; alpha 7 subunit.
                                                                                                                                                                                                                                                     1442 TCGCCACGCTAGCCGTGCTGTCCGCGCCCACATCATGGTGTC 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Human nNAChR alpha 7 subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 101; Column 57-60; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 73..1581
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                                                         TCGACTACGAGCTCTCCCTC---
                                                                                                                                                                                                                                                                                                                                          ABS54875 standard; cDNA; 1876
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92US-0938154.
93US-0028031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MERI ) MERCK & CO INC
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08-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 839; Conserv
                                       Ashkenazi AJ,
                                                    Watanabe CK,
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                                                                  GGGTGCTGCGCATGTCACGGCCCCGGCTCGGCGACGACGCCGCCGCCGCGGCGCGCGTACCTC
                                                                                             GGTTCCTSCGAATGAAGAGGCCCGGGGAGACAAGGTGCGCCCGGCCTGCCAGCACAAGC
                                                                                                                                                     1154 AGCGGCGCTGCAGCCTGGCCAGTGTGAGCGCCGCGTGGCGCCGCCGCCGCCAGCA
                                                                                                                                                                                   ACGTGCTCGACATCGACGACTTCCGCCACCCGCAAGCGCAGCAGCCGCAATGCTGCC
                                                                                                                                                                                                   GAGTCATCACAGATCAGATGCGCAAGGACGACGAAGATGCGGGACATTTCGCGCGCACTGGA
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                                                                                                                           1115 CGCCG------CCGGACCTGGAGCTGCGCGGGCGCTCCTCCAAGTCGCTCCTAGCGA
            <u> ACGCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGCTGCCGT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1514 TCTGCACCATCGGCATCCTGATGTCGGCTCCCAACTTCGTGGAGGC 1559
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99WO-US12252.
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05-JAN-2000;
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Indels

27.2%; Score 404; DB 21; Length 1509; 56.5%; Pred. No. 1.5e-88;

Pred. No. 1.5e 0; Mismatches

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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR0309, PR0314, PR01009, PR06199, PR0317, PR06199, PR0317, PR01009, PR01009, PR01031, PR02034, PR02031,                                                                                                                             ΑĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO polypeptides, useful in the of cancer -
                                                                                                                            Roy
                                                                                                                      Hillan KJ,
                                                                                                                            Gurney AL,
                                                                                                                            Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thirty PRO polynucleotides encoding treatment, diagnosis and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 50; Fig 57; 286pp; English.
                                                                                                                            Baker KP,
                                                                                                                                                                                    Wood WI;
(GETH ) GENENTECH INC.
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AAC90385 standard;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGTCAACGAGGGACCCGCTGCAGCTCTCCTTCGGCCTCACGCTCATGCAGATCATCG
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                                                                                                      Mutant human alpha7 ligand gated ion channel coding sequence #1.
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                                                                                                                                  Human; alpha7 nicotinic acetylcholine gated ion channel;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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Matches 839; Conserv
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                             GCACGTATCCAACGAACGTGGTGCGGAACAACGGCTCGTGTCTGTACGTGCCGCCCG
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Sequence 1509 BP; 298 A; 451 C; 429 G; 331 T; 0 other;
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Pred. No. 1.5e-88;
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                                                                                                                                                                standard; cDNA; 1509
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ilarity 56.5%;
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839; Conserv
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1262 TGCACGGGGGCAACCCCCCGAGGGGGACCCGGACTTGGCCAAGATCCTGGAGGAGGTCC 1321
                                       GCTACATTGCCAATCGCTTCCGCTGCCAGGACGAAAGCGAGGCGGTCTGCAGCGAGTGGA
                                                          AGTTCGCCGCCATGGTCGTGGACAGACTGTGCCTTATTATCTTTACCCTGTTCACAATCA
                     GAGTCATCACAGATCAGATGCGCAAGGACGACGAAGATGCGGACATTTCGCGGCGACTGGA
                                                                                               TCGCCACGCTAGCCGTGCTGTCCGCGCCACACATCATGGTGTC 1487
                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   Wolfe ML,
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P-PSDB; AAB50017.
                                                                                                                                                                                                                         Mutant human alpha7
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838; Conserv
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                                                                                                                                                                                                                                                                        Homo sapiens.
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ATCACTATTTACAGTGGAATGTGTCAGAATATCCAGGGGTGAAGACTGTTCGTTTCCCAG
                                                                CCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACA
                                                                         311 ATGGCCAGATTTGGAAACCAGACATTCTTCTATAACAGTGCTGATGAGGCGCTTTGACG
                                                                                                                GCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCGGAGAAA
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                            ATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCCAC
                                                                                                     GCACGTATCCAACGAACGTGGTGGTGCGGAACAACGGCTCGTGTTTGTACGTGCCGCCCG
                                                                                                                                           GCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACCAACGAT
                                                                                                                                                                                GCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutant;
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Pred. No. 3.7e-88;
0; Mismatches 606; Indels 42;
Human; alpha7 nicotinic acetylcholine gated ion channel;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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                                                                                                                                                                                                               CDNA; 1509
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ilarity 56.4%;
Conservative
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1201

1321 1321 1381 1381

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This sequence encodes the V247T variant of human alpha7 nicotinic acetylcholine receptor (nAChR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 nAChR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating
---ATTCTGAAGGAGATTA
                                                                                                      1226 GATACTACAGGGGGGGGGGGAGAATGGCGGGGGGTTGGCGGCGCGCACAGTTGCTTCGGTG
                                                                                                                                            GAGTCATCACAGATCAGATGCGCAAGGACGACGAAGATGCGGACATTTCGCGCGACTGGA
                                                                                                                                                                 GCTACATTGCCAATCGCTTCCGCTGCCAGGACGAAAGCGAGGCGGTCTGCAGCGAGTGGA
                                                                                                                                                                                              AGTICGCCGCCATGGTCGTGGACAGACTGTGCCTTATTATCTTTACCCTGTTCACAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; canconeurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease; schizophrenia; ss.
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                                                                                                                                                                                                                                                             1442 TCTGCACCATCGGCATCCTGATGTCGGCTCCCAACTTCGTGGAGGC 1487
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                                                                                        1286 TCGACTACGAGCTCTCCTC-
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livan JP, Touma E
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              11 ATGGCCAGATTTGGAAACCAGACATTCTTCTCTATAACAGTGCTGATGAGCGCTTTGACG
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dysfunction, such as cancer, post-herpetic neuralgia, diabetic neurapathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru, psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in stu immuno-fluorescent assay). Compared with wild-type alpha? nAchR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (incotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
  and immune
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Sequence 1590 BP; 322 A; 471 C; 449 G; 348 T; 0 other;

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Title: US Perfect score: 14 Sequence: 1	US-09-303-232-3_COPY_335_1822 1488 1 atggggggggggggcgccgccaçac	.cgccaçacatcatgtgtcg 1488
Scoring table: II	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched: 28	2888711 seqs, 20454813386 residues	
Total number of h	hits satisfying chosen parameters:	5777422
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AF143846 Heliothis AX009612 Sequence E58347 Nucleic aci	46 Drosop 09 Drosop	AF321447 Drosophil AF321445 Drosophil	AF272778 Drosophil AF143847 Heliothis	AX009614 Sequence	AJ55420 Drosophil	AF321448 Drosophil AF321449 Drosophil	AX009610 Sequence	AY036613 Drosophil	AF486623 Macaca mu	AF225980 Mus muscu: AX054567 Sequence	AR282833 Sequence	AX/19088 Sequence U62436 Human nicot	AR055255 Sequence	AR1/1403 Sequence AR1/3187 Sequence	AR224030 Sequence	AX054577 Sequence	Y08420 H.sapiens m	SS398/ nicotinic r AX054579 Sequence	L31619 Rattus ratt	AF385585 Homo sapi N40583 Himan alpha	X70297 H.sapiens m	.sapiens	.caurus m uman a7 n	Sequence	Variant Danio r	AJ000399 Heliothis X52295 Chicken alp	linear INV 27-MAV	acetylcholine recep			poda; Insecta; Pterygota;	trysia;	кі, м.
dı 8	3 AF143846 6 AX009612 6 F58347	AF3214 DME554	AF3214 AF3214		AX0096	DME5542		AX00961	-	AF486623	0								_	0							HVNACHRA1 GGA7NAREC	a629 bd	putative nicoti omplete cds.	.004	(tobacco budworm)	Arthropoda; Hexapoda; Insecta;	gota; Lepidoptera lae; Heliothinae;	Adamczews
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Pred. No. 6.4e-291;
Mismatches 0;
                                                                       Bayer AG,
                                                     and Adamczewski, M
                          subunits
Unpublished
2 (bases 1 to 3629)
Schulte, T., Oellers, N. and Adamcze
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Be
51368, Germany
                                                                                         Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 1488; Conservative 0;
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JP 2000023680-A/2.
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DITWFPPDDQRCEMKFGSWTVDGYQLDLLQDBGGGDISSFYTNGEWELGYPCKRUE
IYYNCCPEPYIDITFAVVYIRKTLYYFFNLLYPCVLIASMALLGFTLPPDSGERLSLG
YTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFWVASSVVSTILILNYHHRAD
THEMSDWRFAAMVVDRANSROSATTPPPARVPPPDLERERSSKSLLANVLD
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Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoneryce; Eukaryota; Lepidoptera; Glossata; Ditrysia;
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                                                                       Adamczewski,M.D., Schulte,T.D. and Oellers,N.D.
Nucleic acids encoding acetylcholin-receptor subunits
Patent: EP 0962528-A 3 08-DEC-1999;
BAYER AG (DE)
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                                                 Noctuoidea; Noctuidae; Heliothinae; Heliothis
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335. .1825
/note="unamed protein product"
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Drosophila melanogaster
Eukaryota; Metazao; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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subunit variant type II
alternatively spliced.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Glossata; Ditrysia; Noctuoidae; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3701)

5 Martin, A., Nadja,E. and Thomas.S.

Nucleic acid encoding insect actyl choline receptor subunit Patent: JP 2000023680-A 2 25-JAN-2000;

BAYER AG

OS Heliothis virescens
PD 25-JAN-2000

PF 26-APR-1999 JP 1999118159

PP 36-APR-1999 DF 1999118159

PP MARTIN ADAMUTSUBUSUKI, NADJA ERASU, THOMAS SCHULTE PC
C12N15/09, A01K67/033, C07K14/705, C07K16/28, C12N15/10, PC
C12L015/08,
PC G01N33/15, G01N33/50//(C12N1/21, C12R1:19), C12N15/00, C12N5/00
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6.4e-291;
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/organism="Heliothis virescens"
/mol_type="genomic DNA"
/db_xref="taxon:7102"
/db_sref="taxon:7102"
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Location/Qualifiers
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100.0%; Pred. No. 6.4
ive 0; Mismatches
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JOURNAL
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SE COUNT S47 a S08 c S03 g 465 t	Db 447 AAGCTGTCAAGGACCTCATGAAAAGCGCCTGCTGAACCATCTGCTGTCCACCTACAATAC 506	QY 261 ACTAGAGTGGAATGATGATGAGCTTGAGGTGGAACACTTCAGATTTCGGCGGGTCAAAGA 320	Qy 381 CGAAGGGTTCGACAGCACGTATCCAACGAAGCTGGTGGTGCGGAACAACGGCTCGTGTCT 440	Db 867 TGATGACCAACATTGCGAAATTCGGTAGTTGGACTTACGAAATCAGTTGGA 926	681 ATACATCGACATCACGTTCCGGTGGTGATCCGGAGGAAACGCTCTACTACTTCTTCAA	QY B01 AGATCCGGAGAAAGTTTAGTGATGATGATTGATTCTTTGATCGTGGGGGTTCTT B60
Ephydroidea; Drosophilidae; Drosophila. (bases 1 to 2023) Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B. Novel Putative Nicotinic Acetylcholine Receptor Subunit Gen Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Id New and Highly Conserved Target of Adenosine Deaminase Actin RNA-Mediated A-to-I Pre-mRNA Editing Genetics 160 (4), 1519-1533 (2002) 21963411 11973307 2 (bases 1 to 2023) Grauso,M. and Sattelle,D.B. Direct Submission	JOUKNAL SUBJITCHED (15.NOY-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OX1 3QX, UK Location/Qualifiers 12023 /organism="Drosophila melanogaster" /db_xref="max"/db	/map="30D1" //dev_stage="embryo" gene 12023 /gene="nAcRalpha-30D" /gene="nAcRalpha-30D" /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b and 8a"	a6 subunit . MHLLSTYNTL WNETEYGGVK KSTCKMDITW KSTCKNTITYA EKLTLGVTIL HHRTADIHEM	KSVFLOWLPWILKMRRCKRITRKTILLSNRMKELELKERSKK, HTSGSQTALGSSASFGRPTTVEHHTALGCNHKDLLILKELQI TJGDWKFAAMVUDRECLIVFTLFTIIATVTVLLSAPHIIVQ" 1794 ne="nackalpha-30D" ce="results in glycine to asparagine substitutare to the sequence deposited in GenBank Active the Sequence deposited in GenBank A	<pre>variation 794 /gene="nAcRalpha-30D" /note="results in glycine to serine substitution; compared to variant clone" /replace="a" variation 846 /gene="nAcRalpha-30D" /note="results in asparagine to serine substitution; compared to the sequence deposited in GenBank Accession</pre>	Number AE005626 and in variant clone" /replace="a" nAcRalpha-30D" /note="compared to variant clone" /replace="a" AACRalpha-30D" /note="compared to variant clone" /replace="compared to variant clone" /replace="t" nAcRalpha-30D" /note="compared to variant clone" /replace="t" replace="t" /replace="t" /replace="t"

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Gaps

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CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
LSLTVFLNLVAESMPTTSDAVPLIGTYFNCIMFWVASSVVLTVVVLNYHRTADIHEM
PPWIKSVFLQWLPWILRMGRPGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDD
DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADD
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/product="nicotinic acetylcholine
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Pred. No. 1.5e-113;
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/gene="nAcRalpha-30D"
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ERPVANESEPELWKFGLTLQQIIDVDEKNQLLTNIGHISLEWDYNLEWNFFFKGGWK
DLRIPWKLWRPDVLMYNSADGEDGTYHTSVVVKGSCLYVPGFFKRGTKRDTW
PPFDDQHCEMKFGSVHTYDGNQLDLVLSSEDGGDLSDFITNGEWYLLAMPGKKNTIVYA
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                                                                                                                                                                                                                                                                                                                                                                                                                   CTACCACCATCGCACAGCGGACATTCACGAGATGCCACCGTGGATCAAGTCCGTTTTTCCT
                                                 CCTAGCGAACGTGCTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCAGCGCAGCGCA
                                                                                                                                                                                                                                                CGCCATTGGCTCGTCGGCCAGCTTCGGTCGGCCCACAACGGTGGAGGAGCATCACACGGC
                                                                                                                                                                                                                                                                                CTTCGGTGTCG----ACTACGAGCTCTCCCTCATTCTGAAGGAGATTAGAGTCATCACAGA
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                                    TTATTGGCTGCCGTGGGTGCTGCGCATGTCACGGCCCGGCTCGGCGACGACGCCGCCGCC
                                                                                              GGCGCGCGTA---CCTCCGCCGCCGGACCTGGAGCTGCGCGAGCGCTCCTCCTAAGTCGCT
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-MAR-2003) Millar N.S., Department of Pha
University College London, Gower Street, London, WCIE
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/db_xref="G1:29466435"
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/mol_type="mRNA"
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44. .1528
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Genetics Unit, University of Oxford,
                                                       /organism="Drosophila m
/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
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379. .1863
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1. .2023
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                                                                          980
                            I (Usase I to Actor)

In (Usase I to Actor)

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Naphpas, Dalphad and Dalpha7, in Drosophila melanogaster Identify

New and Highly Conserved Targed Of Adenosine Deaminase Acting on

RNA-Mediated A-to-I Pre-mRNA Editing

Genetics 160 (4), 1519-1533 (2002)
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                                                                                                                                                                                                               1132 AATACTATTAAGCAATGCCATGAAGGAGCTGGAGCTAAAGGAGGCTCCTCCCAAATCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGATGCGCAAGGACGACGAAGATGCGGACATTTCGCGCGACTGGAAGTTCGCCCCAT
              CAACATGGTGGCGGAGACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTA
                                                                       CTTCAACTGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTGATCCTCAA
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Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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1 (bases 1 to 2023)
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Drosophila melanogaster
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Grauso, M. and Sattelle, D.B.
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CCEBPYVDITFTIOIRRRTLYYFFNLIVPCYLISSMALLGFTLPPDSGEKLTLGVTIL
SLATYFLNLVAETLPQVSD1FLLGTPROTUHFWVASSVVLTVVLNYHHRTADIHEM
PPWIKSYFLQWLPWIILMGRFGRKITRKTILLSNRWKELELKERSSKSLLANVLDIDD
DFRHTISGSGTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARWRKADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDSPLPASLSLEVLLIFLATIKESCOGPHEKRLLNHLLSTYNTL
ERPVANESEPLEVKFGLTLQOIIDVDEKNQLLITNLMLSLEWNDYNLRWNETEYGGVK
DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHSGSCLYVPPGIFKSTCKMDITW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="nAcRalpha-30D"
/note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
South Park Road, Oxford OX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 GCCACGCTGCGGGTACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 CTCGCACTTGGCGGCGCCCCGGGGCCTGCTGCTGCTGTGCCTGCTCTGGCCGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507 GCTGGAGCGACCCGTGGCCAATGAATCGGAGCCCCTGGAGGTTAAGTTCGGACTGACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     567 GCAGCAGATCATCGACGTGGACGAGAAGAATCAGCTTCTCATAACGAATCTTTGGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTAGAGTGGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to serine substitution; com
in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                            /product-"nicotinic acetylcholine receptor Dalpha6 variant type III"
/protein.id="AAM1339.1"
/db_xref="G1:20152849"
                                                                                                                                                                                                                                                                                                                                                   contains exons 3b
                                                                                                                                                                                                                                                                                                                        /note="ion channel; neurotransmitter transmembrane
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                            melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score vir...
Pred. No. 1.5e-113;
                                                                                                                                                                                                                                                                                                                                                   receptor; alternatively spliced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= results in glycine to the sequence deposited AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 611.8;
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INV 29-APR-2002

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/product="nicotinic acetylcholine receptor Dalpha6 subunit variant type I"
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/db_xref="G1:20152845"
/tb_xref="G1:20152845"
/translation="MDSPLPASLSEVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTLERPRANESEPLEVKECHTLOOIDVDEKNOLLTTNAMLNLEWNDYNLEWNEFEYGGVKDLTTPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHNGSCLYVPPGIFKSTCKIDITW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPFDDOHCEMKFGSWTYDGNQLDLVLWSEDGGDLSDFITNGEWYLLAMPGKKNTIVYA
CCPEPYVDTTFTIQIRRRTLYYFFNILIVPCVLISSMALLGFTLPDSGERLTLGVTLL
CZTYVELNLVAETLPQVSDAIPLLGFYFNCIMFWVASSVVLTVVVLNYHHRTADIHEM
PPWTKSVFLQMLPWILLRAGREGKKTPRKTILLSNRKKELELERERSSKSLLANVLDIDD
DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARWRKADD
                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2023)
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Brovel Putrative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
Genetics 160 (4), 1519-1533 (2002)
21969411
11973307
                                                                                                                   ACSOLUTES TO SOURCE TO SOURCE TO THE TOWN SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TO SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN SOURCE TOWN 
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/note="results in isoleucine to methionine substitution;
compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OXI
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                                                                                                                                                                                                                                                                                                                                                                             Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3a
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
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/organism="Drosophija melanogaster"
  GGTGCTCCTCCGCTCCGCATAATCGTG 1857
                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mrNA"
/db_xref="taxon:7227"
/cbromosome="2"
/map="30b1"
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379. .1863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
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                                                                                                                                                                                                                                                                           AF321445.1 GI:20152844
                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
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AUTHORS
TITLE
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PUBMED
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AUTHORS
TITLE
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AF321445
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KEYWORDS
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  CGAAGGGTTCGACAGCACGTATCCAACGAACGTGGTGGTGCGGAACAACGGCTCGTGTCT
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Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
                          CCTAGCGAACGTGCTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCAGCCGCA
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/note="results in asparagine to serine substitution;
compared to variant clone"
/replace="g"
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                                                                                                                                                                       deletion;
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/note="compared to variant clone"
/replace="t"
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Pred. No. 6.7e-113;
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                                    to serine substitution;
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                                                                                                                                                   Length 2907;
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                                                                                                                                               Score 583.8; DB 3;
Pred. No. 7.1e-108;
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NNSSTQILNGLNKHSWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNES
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/note="results in threonine to isoleucine substitution;
compared to B allele"
                                                                   To bases 1 to 2907)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, University of Oxford, South Park Road, Oxford Oxl 3Qx, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of asparagine and serine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="nicotinic acetylcholine receptor Dalpha5
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/note="results in serine, glycine, and asparagine
insertion; compared to B allele"
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/note="compared to B allele"
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
21969411
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/gene="nackalpha-34E"
/note="results in deletion
compared to B allele"
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/note="results in lysine
compared to B allele"
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                                                                                                                                                                                                                                                                                                  /dev_stage="embryo"
1. .2907
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                                                                                                                                                                                                                                                               /chromosome="2
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                                                                                                            TITLE
JOURNAL
                                                                           REFERENCE
                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACAGC
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Pred. No. 4.3e-106;
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Best Local S
Matches 929
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I (bases 1 to 3029)
Schulte, T., Oellers, N. and Adamczewski, M. Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha
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                                                                                                                                                                                                                                                                                                                2472
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                                                                                                      ---CCGGACCTGGAGCTGCGC
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                                                                                                                                                                                                                                                                                                                                              ----TCGACTACGAGCTCTCCCTCATTCTG
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95. 1600
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                                           CCGTGGGTGCTGCGCATGTCACGGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95. .1600
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Schulte,T., Oellers,N.
Direct Submission
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SEPLEVRRGGTLQQIIDVDERNQLLITNIWLSLEWNDYNLRWNDSEXGGVKDLRITPN
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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Patent: EP 0962528-A 5 08-DEC-1999;
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                                                    Mismatches 460;
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                          1227 ATACTACAGGGGGGGGGAGAATGGCGGGGGTTGGCGGCGCACAGTTGCTTCG----
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            GCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGCTGCCGTGG
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Heliothis virescens (tobacco budworm)
Heliothis virescens
Heliothis virescens
Eukaryota; Matazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3109)
Martin,A., Nadja,E. and Thomas,S.
Nucleic acid encoding insect actyl choline receptor subunit
Patent: JP 2000023680-A 3 25-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OS Heliothis virescens
PN JP 200023680-A/3
PD 25-JAR-2000
PP 26-APR-1999 JP 1999118159
PF 04-MAY-1998 DE 19819829.9
PR MARTIN ADAWUTSUEGSUKI. NADJA ERASU, THOMAS SCHULTE PC C12N15/09, A01K67/033,C07K14/705,C07K16/28,C12N1/21,C12N15/10,PC G01N33/15,G01N33/15,G01N33/50/,(C12N1/21,C12R1:19),C12N15/00,C12N5
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    /organism="Heliothis virescens"

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Nucleic acid encoding insect actyl
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/db_xref="taxon:7102"
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                                                                           /product="nicotinic acetylcholine receptor subunit
Dalpha7"
VDRLCLIIFTLFTIIATLAVLFSAPHFIVSGVRG"
                                                                                                                                                   Score 568.4; DB 3;
Pred. No. 9.1e-105;
0; Mismatches 416;
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              26. .131
/gene="nAcRalpha-18C"
132. .1651
/gene="nAcRalpha-18C"
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al Similarity 65.0%;
979; Conservative
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NSSEFGGVRDLAIPPHRLWRFDVLMYNSADBGEGDTYATNVVRNNGSCLYVPRJEK
STGKIDITMPFDDDGXCEMKFGSWYYDFQLDLQLQDEAGGDISSFTNGEWDLAVP
GKRNEIYYNCCPEPYIDITFAILIRRKTLYYFFNLIVPCVLLASMALLGFTLPPDSGE
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/db_xref="GI:29466437"
/translation="MSFPQPHSLPEATANGGRMLVYGLGLLIMIPACAAGPHEKRLLH
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HRNDTHEMSEMIRVIFLYMLPCILRMQRPGOVGYECPPPPSSSSSASGEKKGOLOU
VELKERSSKSLLANVLDIDDFRCHHRCASATLPHQPTYRTHYRQGDGSVGPVGPA
GPVVDGRLHFAISHTCLTSSARYELALILKELMITEGLKKEDETSDITRDMRFAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, University College London, Gower Street, London, WClE 6BT, UNITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DME554210 1683 bp mRNA linear INV 01-APR-20
Drosophila melanogaster mRNA for nicotinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                    AGGATGAGGGAGCTGGAACTGAAGGAGAGGTCGTCGAAGTCCTTGCTGGCGAATGTTCTA
                                                                                           CTGAAGGAGATTAGAGTCATCACAGATCAGATGCGCAAGGACGACGAAGATGCGGACATT
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Drosophila melanogaster
Eukaryota; Wetazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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26. .1654
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/db_xref="taxon:7227"
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Millar, N.S.
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/product="nicotinic acetylcholine receptor Dalpha6 subunit variant type IV"

variant type IV"

protein_id="AaM1395.1"

/db_xref="G152861"

/translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLINHLLSTYNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSSKSLLANVLDIDDDFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLIL
KELQFITARWRKADDEAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERPVANESEPLEVKFGLTLQQ1IDVDEKNQILTTNAMLNLDEKNQLLITNLWLSLEWN
DYNLRWNETEYGGVKDLRITPNKLMKPDVLMYNSADEGFDGTYHTNIVVKRSGSCLYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVLNYHHRTADIHEMPPWIKSVFLQWLPWILRMGRPGRKITRKTILLSNRMKELELKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLLAMPGKKNTIVYACCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="results in methionine to isoleucine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="nAcRalpha-30D"
//note="results in arginine to histidine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="results in serine to asparagine substitution; compared to the sequence deposited in GenBank Accession Number AE003626"
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
                                                                                                                                                                                                                                                                                                                       /note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a, 3b
8b; contains two repeats of the functional domain loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 CTCGCACTTGGCGCGCCCCGCGGCCTGCTGCTGCTGCTGTGCTTTGGCCGAGGGG
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/note="compared to the sequence deposited
Accession Number AE003626"
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Pred. No. 9.1e-102;
0; Mismatches 519;
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Accession Number AE003626
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                                                                      1. .2068
/organism="Drosophila m
/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
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/gene="nAcRalpha-30D"
379. .1908
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/gene="nAcRalpha-30D"
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1. .2068
                                              Location/Qualifiers
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Best Local Similarity 62.4%;
Matches 946; Conservative
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bobtera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilade; Drosophila.

I (bases 1 to 2068)

Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.

Novel Putatrive Nicotinic Acetylcholine Receptor Subunit Genes,

New and Highly Conserved Target of Adenosine melanogaster Identify a

New and Highly Conserved Target of Adenosine Deaminase Acting on

RNA-Mediated A-to-I Pre-mRNA Editing

Genetics 160 (4), 1519-1533 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                              ----CCGCAAGCGCAGCAGCCGCAATGCTGCCGATAC 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1231 TACAGGGGGGGGGAGAATGGCGCGGGGTTGGCGGCGCACAGTTGCTTCGGTGTCGAC 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TACGAGCTC 1299
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                                                                                                                                                                                                                                              1151 TCTTCTTCGAGTTCCTCCGCCATCCGGCGAGAAGAAGCAACAGATCCAAAACGTTGAGCTC 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCAATCATCGATGTGCCAGCGCGACTTTGCCCCACCAGCCCACATATTACAGGACGATG 1330
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AF321448
              CGGCACGCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGCTG
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Grauso, M. and Sattelle, D.B.
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1631 ATTGTG 1636
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AUTHORS
TITLE
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TITLE
JOURNAL
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KEYWORDS
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81 GGCACGCTGCGGGTACCACGAGAAGCGCCTACTGCACCTACTTGGACCACTACAAGCTTCTCTCTTCTCTTCTTCTTCTTTTTTTT	TIGCACCACTATTGGACCACTACAAGGT 140 11 1 1 1 1 1 1 1 1 1	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 GCCGGGGGGGGGCGCGGGGGGGGGGGGGGGGGGGGGG

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                                           CCCGGCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACCAA
                                                                                                   CGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAACTA
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/db_xref="G1:9996843"
/db_xref="G1:9996843"
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SMPPFKTRKSTDTYSTPAATTACPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLH
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NNSSTQILNGLNKHSWIFLLIYINLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNES
DPLQLSFGITLMQIIDVDERNQLLYRVWLKLERPVRNWISDYGGYKDLR IPPR
IMPPDVLMYGNSDEGFDGTYQTNVVVTNNGSCLFWPDRIFKSTGKIDIGHYFPFDDRC
EMKFGSWYYDGFQLDLQLDDFTGGDISSYVLNGEWELLGVPGRRIFYYNCCPEPYID
ITFAIIIRRRTLYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLN
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LSDVELKERSSKSLLANVLDIDDDFRHNCRPWTPGGTLPHNPAFYRTVYGQGDDGSIG
PIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMV
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Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: EP 0962528-A 1 08-DEC-1999;
BAYER AG (DE)
 GGGTACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGTACTGGAGAGG
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Ephydroidea; Drosophilidae; Drosophila
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/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
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Pred. No. 1.7e-93;
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/note="unnamed protein product"
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Eukaryota; Metazoa; Arthropoda;
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Search completed: August 21, 2003, 09:54:17 Job time : 5551.39 secs

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297 IYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 353
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Patent No. 5683912
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ELGOTHEN, ANA BELEN
APPLICANT: JOULTER, JAMES R.
APPLICANT: HEINEMAIN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1465
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Pred. No. 4.3e-107;
80; Mismatches 117;
                                                   US-09-217-345-4
US-08-487-596-18
US-08-464-2588-3
US-08-487-596-4
US-08-288-358-3
US-08-278-6358-3
US-08-487-596-10
US-08-487-596-10
US-08-487-596-10
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US-08-487-596-10
US-08-496-855A-6
US-08-466-589-12
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US-08-467-574-12
US-09-217-345-12
US-08-466-589-10
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46.0%;
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Best Local Similarity 46.08
Matches 240; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
, MOLECULE TYPE: protein US-08-278-6358-7
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MEDIUM TYPE: Floppy
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STREET: 4365 EXEC
CITY: SAN DIEGO
STATE: CALIFORNIA
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/cgn2_6/ptodata/1/iaa/pcvuCs_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcvuCs_COMB.pep:*
                        GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS
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TOPOLOGY:
US-08-464-258B-7
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US-08-471-961-7
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                KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
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APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
                                                                                                                                                                                                                                ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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CLASSIFICATION: 530
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REFERENCE/DOCKET NUMBER: P41 9989
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APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08464258B
Patent No. 6013766
                                                                                                                                                                                                                                                                                                                                                                                                   -----LASVELSAGAG-
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TELEPHONE: 619-677-1409
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APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, SYEBHEN F.
TITLE OF INVENTION: CLONING NEW EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
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                                                                                                                                               Score 1191.5; DB 3
Pred. No. 4.3e-107,
0; Mismatches 117,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: GRAY CARY WARE & FREIDENRICH CITY: 4365 EXECUTIVE DRIVE, SUITE 1600 CITY: SAN DIEGO STATE: CALIFORMIA
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Patent No. 6100046
                                                                                                                                                                                                  80;
                                                                                                                                                  29.5%;
llarity 46.0%;
Conservative 8
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS
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OPERATING SYSTEM:
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OF SEQUENCES:
                                                                                       USA
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                                                                                                                                                COMPUTER:
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                                                                         STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                68 KNQVLTTNIMLQMSWTDHYLQMNMSEYPGVKNVRFPDGQIWKPDILLINNSADERFDATFH 127
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                                                                                                                                                                                                                                                                                                                 Length 502;
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Patent No. 5683912
GENERAL INFORMATION:
APPLICANT: ELGOTHEN, ANA BELEN
APPLICANT: BOULTER, JAMES R.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
APPLICANT: APPLICANT: ACTIVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                         REFERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1465
FORMATION FOR SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SEC
                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
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 US/08/471,961
                                                                                                                                                                                                                                                                                                                                           80;
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                   NAME: REITER, STEPHEN E. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                      : 502 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-471-961-7
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                      linear
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                              CLASSIFICATION:
                                                                                                                                                                                                                                                     TOPOLOGY:
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Best Local Simi
Matches 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 511;
                                                                                                                                                                                                 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1168; DB 1;
; Pred. No. 8.5e-105;
83; Mismatches 117;
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/278,635B FILING DATE: 21-JUL-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,192
REPERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                     1: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.9%;
Best Local Similarity 44.2%;
Matches 238; Conservative 83
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                                                                                                                                                                                                                                                                                                                                          NAME: REITER, STEPHEN E. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 511 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                  CALIFORNIA
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                                                                                665 NPAFYRTVYG------QGDD--GSIGPIGSTRMPDAVTHHTCIKS--STEYELGLI 710
                                                                                                          405 DEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464
                                       ------PG----H 387
605 ILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH 664
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLOWING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
UNDBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR/A77
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44.2%; Pred. No. 8.5e-105;
live 83; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: GRAY CARY WARE & FREIDENRICH 4365 EXECUTIVE DRIVE, SUITE 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-UUL-1994
ATTORNEY/AGENT INFORMATION:
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                                         364 SCKY----SYPKHHPSLKNTEM-
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Patent No. 6100046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                            FORMATION.
T: ELGOYHEN, ANA BELLO.
T: JOHNSON, DAVID S.
T: TOTT TER, JAMES Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
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TELEPHONE: 619-677-1409
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Best Local Similarity 44.2%
Matches 238; Conservative
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; MOLECULE TYPE: protein
US-08-471-961-8
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CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 NGLNKHSWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPYLNESDPLQLSFGLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 100;
                                                                                APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 511;
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.9%; Score 1168; DB 3; 44.2%; Pred. No. 8.5e-105; Live 83; Mismatches 117;
                                                                                                                                                                                                                                                   E: GRAY CARY WARE & FREIDENRICH LLP 4365 EXECUTIVE DRIVE, SUITE 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/POCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                     Sequence 8, Application US/08464258B Patent No. 6013766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 8:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.2
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    CALIFORNIA
                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               SAN DIEGO
                                                                                                                                                                                                                                                        ADDRESSEE:
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US-08-464-258B-8
                                                                                                                                                                                                                                                                                               CITY: SAN
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                         STREET:
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127 DERFONTENTIAL	8-289-8	Query Match 28.7%; Score Best Local Similarity 45.1%; Pred. Matches 237; Conservative 82; Mis	QY 297 IYENLSAKVCLAGYHEKRLLHDL :: : :: : Db 8 WALALAASLLHVSLQGEFQRKLYKEL	. 354	DD 68 KNQVLTTINIWLQMSWTDHYLQWNVSE	Qy 414 TNVVVRNNGSCLYVPPGIFKSTCKID	Qy 474 GDISSYVLNGEWELLGVPGKRNEIYY		Qy 534 ASMALLGFTLPPDSGEKLSLGVTILL :::	582	305	613 CSDTSSERKH	Db 364 CSLASVEMSAVAPPPASNGNI		Qy 724 DDECNDIANDWKFAAMVVDRLCLIIF	Db 450 QDESEAVCSEWRFAACVVDRLCLMAF	RESULT 8	Sequence 8, Application US/08700636	; Patent No. 5910582 ; GENERAL INFORMATION:	; APPLICANT: Elliot, Kathryn J. ; APPLICANT: Ellis, Steven B.	; APPLICANT: Harpold, Michael M. ; TITLE OF INVENTION: HUMAN NEURONAI	; TITLE OF INVENTION: RECEPTOR COMPO ; NUMBER OF SEQUENCES: 12	; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Pretty, Schroeder, Br	STREET: 444 South Flower Street,	TE:	; ZIP: 90071 ; COMPUTER READABLE FORM:	COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPANDED CO	' :	APPLICATION NUMBER: US/08/700, 63 FILING DATE: 16-JUL-1996	CLASSIFICATION: 536 PRIOR APPLICATION DATA:	APPLICATION NUMBER: US 08/028,03
0) 1 0) 11		465 DLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFF 52 	525 NLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 58	244 NLLIPCVLISGLALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQ	304 YPASIMVIVGLSVVYTVLVLOFHHHDDOAGKMPRVYTI.I	605 ILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH ::	364 SCKYSYPKHHPSLKNTEMNVL	665 NPAFYRTVYGOGDDGSIGPIGSTRMPDAVTHHTCIKSSTEVELGLI STEVELGLI 388 QPSNGNMIYSYHTMENPCCPQNNDLGSKSGKITCPLSEDNEHVQKKALMDTIPVIVKI	711 LKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTWFAILATIAVLLSAPHII 		SULT 7 -08-466-589-8	Sequence 8, Application US/08465589 Patent No. 5837489	GENERAL INFORMATION: APPLICANT: Elliot, Kathryn J. APPLICANT: Filis & Serven R	APPLICANT: Harpold, Michael M. TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE	ITIONS AND METHODS EMPLOYING	Haller	CTTY: San Diego STATE: CA COUNTRY IISA	ZIP: 92101-2926	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette	tible OS	sion 1.5 :	S/08/466,58 1995	CLASSIFICATION: 536 PRIOR APPLICATION DATA:	APPLICATION NUMBER: US 08/028,031 FILING DATE: March 8, 1993	ATTORNEY/AGENT INFORMATION: NAME: Seidman, Stephanie L	REGISTRATION NUMBER: 33,779 REFERENCE/DOCKET NUMBER: 6362-9950	TELECOMMUNICATION INFORMATION: TELEPHONE: 619-238-0999 THIPPAX: 619-238-0062	TELEGRAPH OF CENTROL O	cs: cids		, E <u>i</u>
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:LVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDE 67
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SEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFH 127
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||: ||||| | |::|||||: ||:||:||:
|TDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE--- 184
                                                                                                                                                                                                                                                      SLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF 668
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POSITIONS AND METHODS EMPLOYING SAME
e 1159.5; DB 2; Length 502;
No. 5.6e-104;
ismatches 115; Indels 91; Gaps
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aFSVFTIICTIGILMSAPNFV 494
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                                                                                                                                                                                                                                                                                                                                                                                         354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYO 413
                                                                                                                                                                                                                                                                                                                                                                                                           68 KNQVLTINIWLQMSWIDHYLQWNVSEYPGVKIVRFPDGQIWKPDILLYNSADERFDATFH 127
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GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIPCVLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5: Brown, Martin, Haller & McClaim
1660 Union Street
             NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEPHONE: 619-546-3992
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08467574
Patent No. 6022704
                                                                                                                                                                                                                                                         Query Match 28.7%;
Best Local Similarity 45.1%;
Matches 237; Conservative 8
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1000
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------DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.7%; Score 1159.5; DB 3; 45.1%; Pred. No. 5.6e-104; tive 82; Mismatches 115;
                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEPHAX: 610-238-0999
                                     COMPUTER: IBM Compatible.
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILLING DATE: MARCH 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
                                                                                                                                                                                                                                                                            NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 45.1
Matches 237; Conservative
                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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us-09-303-232-2.rai

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305 GLSVVVTVIVLQYHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKORR 363
                                                                                                                                                                                                                                                        245 SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 304
                                            --WIRIVELCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                    613 CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                                                                                                                           669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                                                                                                                                                                   364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP--
                                                                                                                                                                                                                                                                                                                     724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Steven B.
APPLICANT: Elliot, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i: Brown, Martin, Haller & McClain
1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-NAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,455
APPLICATION NUMBER: US 07/504,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08487596 Patent No. 6440681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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                                                                                  APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 IYLNLSAK---VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Seidman, Stephanie L
REGISTATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/467,574
FILING DATE: 05-UNN-95
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
                Sequence 8, Application US/09217345 Patent No. 6303753
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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TELEFAX: 619-587-5360
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LENGTH: 502 amino acids
TYPE: amino acid
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Best Local Similarity 45.15
Matches 237; Conservative
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unknown
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82; Mismatches 116;
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20-JUN-1995
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08-MAR-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/028,C
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seidman, Stephanie
 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 92101-2926
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US-08-496-855A-2
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TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
FILE REFERENCE: 6017.US.01
CURRENT APPLICATION NUMBER: US/08/771,737
UNIMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                  353
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                                                                   Length 502;
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                                                               ; Score 1159.5; DB 4;
; Pred. No. 5.6e-104;
82; Mismatches 115;
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Pred. No. 1.4e-103;
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Patent No. 6323000
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APPLICANT: Roch, Jean-Warc
APPLICANT: Sullivan, James P.
APPLICANT: Touma, Edward
APPLICANT: Abbott Laboratories
                                                                 28.7%;
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APPLICANT: Briggs, Clark A.
APPLICANT: Gopalakrishnan, Mt
APPLICANT: McKenna, David G.
                                                                                  al Similarity 45.1
237; Conservative
                 ; MOLECULE TYPE: protein US-08-487-596-12
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   unknown
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Best Local Similarity
   TOPOLOGY:
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                                                                 Query Match
Best Local S
Matches 237,
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                                                                                                                                                                                                                                             67
                                                                                                                                                       Sequence 2, Application US/08496855A
Patent No. 5801232
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                -----RIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                          474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
  Gaps
91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
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                                                                                                                                                                                                                                            309 GYH---EKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWLK
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                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                    75;
                                                                                                                                                                                        DB 1; Length 529;
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APPLICANT: Elliot, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
                                                                                                                                                                                   21.0%; Score 848.5; DB 1; Length 36.7%; Pred. No. 1.1e-73; ive 87; Mismatches 154; Indels
              6362-9369B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08487596
Patent No. 6440681
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | : | : | : | 503 IFLWLFIIVCFLGTIGLFL 521
33,779
                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                     TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 1660 Union Street
San Diego
                                                                                                 : 529 amino acids
amino acid
REGISTRATION NUMBER: 33
                                                                                                                                                                                                 Best Local Similarity 36.7
Matches 183; Conservative
                                                                                                                           TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-496-855A-2
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US-08-487-596-2
                                                                                                 LENGTH:
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                                                                                                                  TYPE:
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                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: O7-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.0%; Score 848.5; DB 4;
Best Local Similarity 36.7%; Pred. No. 1.1e-73;
Matches 183; Conservative 87; Mismatches 154;
                                                                                                                                                                      FILING DATE: 07-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-WOV-1993
PRIOR APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE-DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEO ID NO: 2:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-596-2
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
READABLE FORM:
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                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 GYH---EKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 848.5; DB 4;
; Pred. No. 1.1e-73;
87; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Fasteso Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                              Sequence 2, Application US/08660451A
Patent No. 6524789
GENERAL INFORMATION:
APPLICANT: Blliott, Kathryn J.
APPLICANT: Harpold, Michael M.
                                    744 LCLIIFTMFAILATIAVLL 762
                                                           : | : | : | : | 503 IFLWLFIIVCFLGTIGLFL 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619-238-0062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
453 ALLQEGELLLSPH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                       APPLICANT: Harpold,
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                         San Diego
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ORIGINAL SOURCE:
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                                                                                                                             RESULT 15
US-08-660-451A-2
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STATE: C.
COUNTRY:
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us-09-303-232-2.rspt

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Q8ipe2 drosophila
Q9vjt9 drosophila
Q9jhd6 mus musculu
Q03481 gallus gall
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081753 drosophila

081713 drosophila

081719 drosophila

09x214 heliothis v

081750 drosophila

09179 drosophila
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drosophila
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Q8t5f5 drosophila
                                                              (without alignments)
2698.100 Million cell updates/sec
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                                                                                                          1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770
                                                    August 13, 2003, 15:21:20 ; Search time 73.6446 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                       830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                    - protein search, using sw model
                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Q03481
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Q8T7S1
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Q8T7S0
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
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sp_bacteriap:*
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seq length: 2000000000
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: sp_bacteria:*
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sp_rodent:*
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O18394 drosophila
Q8t5f4 drosophila
Q8vhh6 mus musculu
                                                         O8t0y9 aplysia cal
O46134 locusta mig
P91764 myzus persi
O9nfx8 myzus persi
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drosophila
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096632 b
096632 b
0840y9 e
046134 b
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Q8mur0
Q46133
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O46128
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Q91X60
Q8WRS1
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Q18556
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ALIGNMENTS

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PRESULT 1

ORT7V5; PRELIMINARY; PRT; 807 AA.

ORT7V5;

ORT7V5;

ORT7V5;

ORT7V5;

ORT7V5;

ORT7V5;

ORT7V5;

ORT7V5;

ORT7V6;

ORT7V6;

ORT7V6;

ORT7V75;

ORT8-2002 (TFEMBLrel. 21, Last sequence update)

ORT8-2003 (TFEMBLrel. 23, Last amnotation update)

ORT8-2003 (TFEMBLrel. 23, Last amnotation update)

ORT8-2003 (TFEMBLrel. 23, Last amnotation update)

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ORT8-2003 (TFEMBLREL. 23, Last amnotation update)

ORT8-2003 (TFEMBLREL. 23, LAST 2003)

ORT8-2003 (TFEMBLREL. 23, LAST 2003)

ORT8-2003 (TFEMBLREL. 23, LAST 2003)

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1 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
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IONIC CHANNEL FAMILY.
                                                                                                 MEDLINE-21969411; PubMed=11973307; Grauso M., Reenan R.A., Culetto E., Sattelle D.B.; Grauso M., Reenan R.A., Culetto E., Sattelle D.B.; Datative Nicotinic Acetylcholine Receptor Subunit Genes, Dalphas, Dalphas, and Dalpha7, in Drosophila melanogaster Identify Mew and Highly Conserved Target of Adenosine Deaminase Acting on Related A-to-1 Pre-mRA Editing."; Genetics 160:1519-1533(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 482;
                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02931; Neur_chan_LBD; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
Endopterygota; Diptera; Brachycera; Muscomorpha; a; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Last annotation update)
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                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED
                                                                                                                                                                                                                                                                                      EMBL; AY036613; AAK67256.1; -.
FlyBase; FBgn0028875; nAcR-alpha-34E.
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InterPro; IPR006202; Neur_chan_LBD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 AA;
                                                                                    SEQUENCE FROM N.A.
                       Ephydroidea; Dro:
NCBI_TaxID=7227;
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Q9VWI9;
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                                                                                                        1 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
                                            Gaps
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1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha5 subunit.
NACR-ALPHA-34E OR NACRALPHA34E OR BG:DS05899.4 OR BG:DS05899.5 OR
654498 OR CG16879.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
    Length 807;
                                          Indels
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    DB
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    Score 4014.5;
Pred. No. 0;
                                            Mismatches
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Q8T5F5;
01-JUN-2002 (TFEMBLFel. 21,
01-JUN-2002 (TFEMBLFel. 21,
01-MAR-2003 (TFEMBLFel. 23,
  99.3%;
95.4%;
                                            Conservative
                       Similarity
                     Local Similar
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Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.T., Busam D.A.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.C., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Perritera S., Frise B., Galle R.F., Gasty N.S., George R.A.,

A Perritera S., Frise B., Galle R.F., Gasty N.S., George R.A.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Potanoon S., Pittman G.S., Patel S., Richards S., Scheeler F.,

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"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
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                  Venter C.J.;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative nicotinic acetylcholine receptor alpha 7-1 subunit.
Heliothis virescens (Noctuid moth) (Owlet moth).
                                                                                                                                                                                                                                                                                                                                                                     Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                Celniker S.E., Gibbs R.A., Rubin G.M., Vente
ARR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                             FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
EMBL, AE003511; AAF48950.2;
                                                                                                                                                                                                                                                                                                                              7B83025107A66209 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   49.2%; Score 1988; DB 5; 71.0%; Pred. No. 7.3e-163; tive 46; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 AA.
                                                                                                                                                                                   InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neur_chan_LBD: 1.
Pfam; PF02931; Neur_chan_LBD: 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
FROSTIE; PS00236; NEUROTR_LON_CHANNEL; 1.
SEQUENCE 545 AA; 61517 MW; 7B83025107A66
                                                                                                                                                    FlyBase; FBgn0031014; nAcR-alpha-18C.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                         Matches 384; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                      (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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Best Local &
                      Adams M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schulte T., Oellers N., Adamczewski M.;
Schulte T., Oellers N., Adamczewski M.;

"Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than
to other insect nicotinic acetylcholine receptor alpha subunits.";

L. Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
REMBL, ART13846; AAD32697.1; -
RINTERPO; IPRO06201; Neur_channel.
R InterPro; IPRO06202; Neur_channel.
R Fam: PF02931; Neur_chan_LBD.
R Pfam: PF02931; Neur_chan_LBD.
R Pfam: PF02932; Neur_chan_mbb.
R PRINTS; PR00252; NRICHANNEL.
                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                              DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRILYYFFNLIIPCVLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                                                                                                                    NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --WIRIVFLCWLPWILRMSRPG---RPLILEFPTTPGS
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                   Receptor;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                      496 AA; 56347 MW; 8032FED8515A6210 CRC64;
                                                                                                                                                                                                                                 Glycoprotein; Ionic channel; Postsynaptic membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIVS 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                          45.8%; Score 1850; DB 5; 70.0%; Pred. No. 5.3e-151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                             30; Mismatches
                                                                                                                                                                                                                       PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                                                                                                             TIGR00860; LIC; 1
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                    Similarity
                                           [1]
SEQUENCE FROM N.A.
                                NCBI_TaxID=7102
                                                                                                                                                                                                                                           ransmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08T7S2
Q8T7S2;
01-JUN-2002 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                             361;
                                                                                                                                                                                                             TIGRFAMS;
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                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                    Best Local
Matches 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 SLFVLLIFLATIKESC-OCPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIID
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                                                                                                                                                                                                     ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                     II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Length 494;
                                                        Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 FMVASSVVLTVVVLNYHHRTADIHEMPPWIKSVFLQWLPWILRMGRPGRKI-
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant ty
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.2%; Score 1625.5; DB 5; 61.4%; Pred. No. 1.3e-131; ive 47; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR006201; Neur_channel.
Interpro; IPR006202; Neur_chan_LBD.
Interpro; IPR006029; Neu_channel_memb.
                                                                                                                                                                                        MEDLINE=21969411; PubMed=11973307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56048 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.2%,
Best Local Similarity 61.4%,
Matches 320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494 AA;
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTVYGQGDDGSIGPIGSTRMPDAV-THHTCIKSSTEYELGLILKEIRFITDQLRKDDECN 728
                                                                                                                                                                          ς
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21969411; PubMed-11973307; Grauso M.; Reenan R.A., Culetto E., Sattelle D.B.; Reenan R.A., Culetto E., Sattelle D.B.; Movel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing."; Genetics 160:1519-1533(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNNVAETMPATSDAVPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDTSSERKHQILS----DVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AF321445; AAM13392.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79;
                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Cphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.1%; Score 1622.5; DB 5; Length 61.2%; Pred. No. 2.3e-131;
ive 46; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 AA; 56095 MW; B46EBEDA63A92942 CRC64;
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                                  464
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006201; Neur_channel.
InterPro; IPR006502; Neur_chan_LBD.
InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
IIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0032151; nAcR-alpha-30D.
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity 61.2
319; Conservative
                                  PRELIMINARY;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470
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                                                                                                                                                                                                                                                   351 VDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 494;
                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophillade; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                     NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
56113 MW; 48327537229573FF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.1%; Score 1620.5; DB 61.0%; Pred. No. 3.5e-131 tive 49; Mismatches 75
                                                                                    Ą.
                                                                                    494
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InterPro; IPR006202; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PIGREPMS; IIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006201; Neur_channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 61.0%
Matches 318; Conservative
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 AA;
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01-JUN-2002 (
01-MAR-2003 (
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                                                                                  Q8T7S1
Q8T7S1;
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700 KSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIA 759
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                                                                                                                          309 TVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEMPPWIK
                                                                                                                                                                                           585 IVFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQILS----DVELKERSSKSLLA
                                                                                                                                                                                                                                                                                                                NYLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAV-THHTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006029; Neu_channel_memb.
Patan, PF02331; Neu_chan_LBD; 1.
Pram; PF02332; Neu_chan_LBD; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRRPMS; TIGRR00869; LIC; 1.
PROSTIE: PS00236; NEUROTR_ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative nicotinic acetylcholine receptor alpha 7-2 subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heliothis virescens (Noctuid moth) (Owlet moth).
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Interpro; IPR006202; Neur_chan_LBD
                                                                                                                                                                                                                            415 NVLDIDDDFRHTI------
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Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      760 VLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7102;
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                                                                                                                                                                     RTVYGQGDDGSIGPIGSTRMPDAV-THHTCIKSSTEYELGLILKEIRFITDQLRKDDECN 728
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophia melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Clesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomontan M.A., Mazda P., Noshrefi A.R., Moshrefi M.,
Nixon K., Paoleb J.M., Park S., Pfelffer B., Poon L., Squeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AEG03408; AAF44854.1, ..
Flybase; Fbgr00228975; nAcR-alpha-34E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Harzell G., Harvey D.,
Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K
Celniker S., Rubin G.M.;
An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster the Adh region.";
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 44.0 kDa protein.
NACR-ALPHA-34E OR BG:DS05899 4 OR BG:DS05899.5 OR CG4498 OR CG16878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE-99403001; PubMed=10471707;
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MEDLINE-21969411; PubMed-11973307;

A Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

The analysis of the control of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of the component of th
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                    DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIA
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087750;

01-JUN-2002 (TrEMBLrel. 21, Created)

01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

01-JUN-2003 (TrEMBLrel. 23, Last annotation update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Nicotinic acetylcholine receptor Dalpha6 subunit variant type I

NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

CBL_TAXID=7227;
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Pred. No. 1.4e-129;
8; Mismatches 76; Indels
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RESTAINBERKELEY;

RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Annantides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.E.,

RA Annantides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA Anton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Aril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Aril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Perriera S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraza C., Ferriera S., Fleischmann R.,

RA Godek A., Gong F., Gorrell J.H., Gu Z., Genbart W.M., Glasser K.,

RA Hostin D., Houston K.A., Hewland T.J., Hernandez J.R., Houck J.

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTQQPTNIRLCARKRQRLRRRRRRRRPATPNETDIKKQQQLSMPPFKTRKSTDTYSTPAAT 180
                                                                                                                                              09
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                                                                                                                                                                                                                                                                  TSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLHVLQVLLVSLQQWQLHVQQRSVL
                                                                                                                                            1 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
                                                                                                                                                                                                                                          HSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA
                                                                                                Gaps
                                                                                                5;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last annotation update)
CG4128 protein.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TAXID=7227;
                                              Length 391;
                                                                                                Indels
  E2AB465CF275E8C0 CRC64;
                                  ;; Pred. No. 4.2e-121; 5; Mismatches 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 NLSAKGECHLNYLECCMQH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLSAK-VCLAGYHEKRLLH 317
43974 MW;
                                                                  94.48;
                                                 37.28;
                                                                     Best_Local Similarity 94.4
Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
391 AA;
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SEQUENCE
                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                    61
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                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                181
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
M. Ye J., Yeh R.-F., Zaveri J. S., Zhan M., Zhang S., Yao Q.A.,
A thiliams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A thiliams S.M., Woodage T., S., Zhan M., Zhang G., Zhao Q., Zhao G.,
A the genome sequence of Drosophila melanogaster.",
Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 VDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burzon J., An H., Baldwin D., Barzon J., Beson K.Y., Busam D.A.,
A Banzon J., An H., Baldwin D., Banzon J., Beson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
Nacincosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
A phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 SLFVLLIFLAIIKESC-QCPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 VDEKNOLLITULWLSLEWNDYNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berrana B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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PROSITE; PSO0236; NEUROTR_ION_CHANNEL; 1.
SROHENCE 554 AA; 63236 MW; D6C63EB7F5B32A35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.4%; Score 1310.5; DB 5;
47.9%; Pred. No. 2.4e-104;
tive 48; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006201; Neur_channel.
InterPro; IPR006029; Neu_channel_memb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBqn0032151; nAcR-alpha-30D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 32.4%
Best Local Similarity 47.9%
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Rapandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlow R.M., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baus A., Baxendale J., Brokstein P., Borshakov S.,
Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Rockova D., Botchan M.B., Butler H., Cadjeu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dourbin K.J. Evangelista C.C., Ferraza C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A Harris N.L., Harvey D., Heinann F.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Weil M.H., Ibbeyam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Hostin D., Houston K.A., Howland T.J., Weil M.H., Ibbeyam C.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Rimmel B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
Rako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Rako P., Lei W., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                        653
597
                                                                                                                                                                                                                                                                                                                                           353 VSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEMPPWIKSVFLQWLPWILRM 412
                                                                                                                                                                                                                                                                                                                                                                                                        654 RPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAV-THHTCIKSSTEYELGLILK 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          713 EIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFALLATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 DNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQCRAERVTILLSLTVFLNLVAETLPQ
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                                                                                                                                         RRRTLYYFFNLIIPCVLIASM------ALLGFTLPPDSGE--------
                                                                                                                                                                                                                           -----KLSLG------VTILLSLTVFLNMVAETMPA
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
CG4128-PC.
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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Revans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
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Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Rapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
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Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AE003626; AAN10709.1; -. SEQUENCE 525 AA; 60135 MW; CF95283C56EA90A9 CRC64;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Favans C.A., Galle R.E.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
RA Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Maril J.F., Agbayani, A., An H. J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani, A., An H. J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,
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RA Borkova D., Botchan M.R., Bouck J., Broketen P., Brottier P.,
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Cabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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Liu X., Mattei B., McIntosh T.C., Morris J., Moshrefi A.,
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RA Rainzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rabanzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Raben H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Rhenert R., Shen B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR
CG4498 OR CG16878.
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Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta; Pterygota;
Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha;
Ephydroidea: Drosophilidae: Drosophila.
NCBI_TaxID=7227;
RRRTLYYFFNLIIPCVLIASM-----ALLGFTLPPDSGEKLS-
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=20196006; Pubmed=10731132;
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Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A.,
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Sun E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
SEQUENCE 273 AA; 31655 MW; CA95F19953E37248 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.3%; Score 1186; DB 5
57.2%; Pred. No. 5e-94;
ive 13; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0028875; nAcR-alpha-34E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan_LBD.
                                                                                                                                                                                                 Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003642; AAF53374.2;
HSSP; P58154; 119B.
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Submitted (SEP-2002)
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Best Local Similarity
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                                                                                                                                                                                       |------SEWLRKDDECNDIANDWKFAAWVVDRLCLIFTWFTLLATIAVLLSAP 268
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LIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLWIRI 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stitzel J.A.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
Stitzel J.A.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
C. -: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR MGJ: MGI:99779; Chrna7.
DR InterPro; IPR006202; Neur_channel.
DR InterPro; IPR006202; Neur_chan.LBD.
DR InterPro; IPR006202; Neur_chan.LBD.
DR Fiam; PF00931; Neur_chan.LBD; 1.
DR Pfam; PF00931; Neur_chan.memb.; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
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                                                       586 VFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDI
                                                                                                               646 DDDFRHNCRPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEY
                                                                                                                                            ELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 IYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stitzel J.A., Farnham D.A., Collins A.C.;
"Linkage of strain-specific nicotinic receptor alpha 7 subunit
restriction fragment length polymorphisms with levels of alpha-
bungarotoxin binding in brain.";
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PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.3%; Score 1185.5; DB 11; Lengt
46.6%; Pred. No. 1.3e-93;
ive 79; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C9353E5136D620E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nicotinic acetylcholine receptor subunit alpha 7.
CHRNA7.
                                                                                                                                                                                                                                                                                                                                    502 AA
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                                                                                    ---- FILLNY ----
                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=97189245; PubMed=9037516;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56617 MW;
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                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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es 243; Conserv
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526
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613 CSDTSSERKHQILSDVELKERSS-KSLLANVLDIDDDFR----HNCRPMTPGGTLPHNPA 667
TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                   474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                             534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                                                                     ---WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CS-----IASVELSAGAGPPSSNGNLLYI--GFRGLEGMHCAP-TP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 SEVICSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            727 CNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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Search completed: August 13, 2003, 15:29:07 Job time: 76.6446 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 15:14:55; Search time 16.1234 Seconds (without alignments) 2245.843 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-303-232-2 4043 1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIIMMARIES

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	ption	mus musculu	qall	rattus	homo sapien	bos t				schistocerc	homo sapien	homo sapien		drosophila	gallus	gallus	gallus	rattus			carassius a					homo sapien	mus musculu	xenopus lae	rattus norv	caenorhabdi				brachydanio
•	Description	P49582	P22770	005941	P36544	P54131	P48180	P09478	P91766	P23414	Q15822	P32297	P17644	P04755	P09480	P09479	P09481	P12389	P04757	007263	P18845	P25162	P30926	P49581	P02709	015825	P04756	P05377		P45963		15	8	088880
SUMMARIES	ID	ACH7_MOUSE	ACH7_CHICK	ACH7_RAT	ACH7_HUMAN	ACH7_BOVIN		ACH1_DROME	ACH1_MANSE	ACH1_SCHGR	ACH2_HUMAN	ACH3_HUMAN	ACH2_DROME	ACH3_DROME	ACH2_CHICK	ACHA_CHICK	ACH3_CHICK	ACH2_RAT	ACH3_RAT	ACH3_BOVIN	ACH3_CARAU	ACH4_DROME	ACHP_HUMAN	ACH6_CHICK	ACHA_BOVIN	ACH6_HUMAN	ACHA_MOUSE	ACH2_XENLA	ACH6_RAT	ACH8_CAEEL	ACHA_RAT	ACHP_CHICK	ACHN_CHICK	ACHA_BRARE
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dР	Query Match								21.9												20.3	20.2	19.9	19.9	19.8	19.8	19.7	19.7	19.6	19.6	19.5	19.5	19.5	19.5
	Score	1182.5	1179.5	1173.5	1159.5	1157	1104	888	886	873	848.5	845	843.5	840	838	827.5	827.5	827	823	820.5	820.5	815.5	802	803	801	799	797			791.5	ന	m	78	786.5
ı	Result No.	1	~	m	4	w.	ا ک	7	ω .	ָה ק	01	11	12	EI ;	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P02711 torpedo mar	P12390 rattus norv	P17787 homo sapien P02708 homo sapien	P43681 homo sapien	P09482 gallus gall	P02710 torpedo cal	P22456 xenopus lae	P12391 rattus norv	P19370 carassius a	P09483 rattus norv
ACHA_TORMA	ACHN_RAT	ACHN_HUMAN ACHA_HUMAN	ACH4_HUMAN	ACH4_CHICK	ACHA_TORCA	ACH1_XENLA	ACHO_RAT	ACHN_CARAU	ACH4_RAT
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461	500	502 482	627	622	461	457	464	459	630
19.4	19.4	19.3	19.3	19.3	19.3	19.1	19.1	19.0	19.0
785	782.5	787	780	779.5	779	773.5	772	769.5	768
3.5	36	38 38	39	40	41	42	43	44	45

ALIGNMENTS

us-09-303-232-2.rsp

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                                                                                                                                                                                                                                                                                                         68 KNQVLTTNIWLQMSWTDHYLQWNMSEYPGVKNVRFPDGQIWKPDILLYNSADERFDATFH 127
                                                                                                                                                                                                                                                                                                                                            114 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
                                                                                                                                                                                                                                                                                                                                                            581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     673 YGQ-----GDDGSI-GPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDE 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 EGMHCAPTPDSGVVCGRLACSPTHDEHLMHGTHPSDGDPDLAKILEEVRYIANRFRCQDE 452
                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                     297 IYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                    534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE-91097796; PubMed-1702646;
Coutunier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,
Millar N., Valera S., Barkas T., Ballivet M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                    POTENTIAL.

BY SIMILARITY.

ASSOCIATED WITH RECEPTOR ACTIVATION

(BY SIMILARITY).
                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
C9312E5226D120E3 CRC64;
                                                                                                                                                                                                           85;
                                                                                                                                                                                DB 1; Length 502;
                                                                                                                                                                                                          80; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNDIANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 SEVICSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                              Pred. No. 2.8e-75;
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                                                                                                                                                                              29.2%; Score 1182.5;
                             POTENTIAL
                                                                                                                                                   56631 MW;
                                                                                                                                                                                              45.8%;
                                                                                                                                                                                                          239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                      490
164
213
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90
133
                                                                                                                                                   502 AA;
                                                                                                                                                                                           Similarity
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 231
262
296
318
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90
133
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P22770;
TRANSMEM
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TRANSMEM
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DISULFID
DISULFID
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                                                                                                             CARBOHYD
                                                                                                                           CARBOHYD
                                                                                                                                        CARBOHYD
                                                                                                                                                     SEQUENCE
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                                          DOMAIN
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neuronal nicotinic acetylcholine receptor subunit (alpha 7) is relopmentally regulated and forms a homo-oligomeric channel blocked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE-85270494; PubMed=3860855;
Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
                                                                                                                                                                                                                                                                                                                                                                                               "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor promoter develops during morphogenesis of the central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brain and muscle nicotinic acetylcholine receptors are different but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-92049732; PubMed=1719423; Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C., Hussy N., Bertrand S., Ballivet M., Changeux J.-P.; "Mutations in the channel domain alter desensitization of a neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC. MEDILINE-93024917; PubMed=1383829; Galzi J.-L., Deviller-Thiery A., Hussy N., Bertrand S., Changeux J.-P., Bertrand D.; Mutations in the channel domain of a neuronal nicotinic receptor convert ion selectivity from cationic to anionic."; Nature 359:500-505(1992).
                                                                                                                                                                   Lindstroem J.;
and MAbs reveal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHABUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                       Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M.,
                                                                                                                                                        Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstroem J. Brain alpha-bungarotoxin binding protein cDNAs and MAbs reve subtypes of this branch of the ligand-gated ion channel gene superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologous proteins.";
Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
                                                                                                                                                                                                                                                                                                                STRAIN-White leghorn; TISSUE=Erythrocyte;
MEDLINE-93049204; PubMed-1425587;
                   developmentally regulated and forms
                                                                                                                                           MEDLINE=90315158; PubMed=2369519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 11:4529-4538(1992).
                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-18 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nicotinic receptor.";
Nature 353:846-849(1991).
                                       alpha-BTX.";
uron 5:847-856(1990)
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PDB; 1KC4; 17-APR-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 24-47.
                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRTLYYFFNLIIPCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532 LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-----
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                                                                                                                                        NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                          75; Gaps
                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
L->S,T: SUPPRESSES INHIBITION BY THE OPEN-CHANNEL BLOCKER QX-222.
QR -> ET (TN DEN.
                                                                                                                                                                                                                                            ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 502;
    InterPro; ITRR006202; Neu_channel_memb.
InterPro; IPR006202; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRIGRAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL, 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL, 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL, 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL, 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL, 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL, 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL, 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL, 1.
                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 4.6e-75;
80; Mismatches 127; Indels
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572325D4309AD2FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.2%; Score 1179.5; 45.7%; Pred. No. 4.6e
                                                                                                                                                              EXTRACELLULAR
                                                                                                                                                                                                                                    SIMILARITY
                                                                                                                                                                                                              CYTOPLASMIC.
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237; Conservative
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502 AA;
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                                                                                                                                Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BÝ SIMILARITY.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hartley M.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                  TISSUE-Brain;
MEDLINE-93147931; PubMed=7678857;
MEDLINE-93147931; Patrick J.W.;
Medicle J., Dineley-Miller K., Dani J.A., Patrick J.W.;
Medicular cloning, functional properties, and distribution of rat
brain alpha 7: a nicotinic cation channel highly permeable to
                              01 FEB-1994 (Rel. 28, Created)
1-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHABUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRRAMs; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CH
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PIR; T01378; T01378 in T01378 interPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PP02931; Neur_chan_LBD; I.
Pfam; PP02931; Neur_chan_memb; I.
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PRT;
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                                                                                                  CHRNA7 OR ACRĀ7.
Rattus norvegicus (Rat).
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502
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                     NCBI_TaxID=10116;
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ACH7_RAT
Q05941;
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TISSUE-Hippocampus; Logel J., Drebing C., Barnhart M., Antle C., Leonard S.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.

FROM N.A.

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                                                                                                                         SALALLVFLIPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV
                                                                                                                                                                                                                                                                                                                   305 GLSVVVIVIVLRYHHHDPDGGKMPKWTRIILLNWCAWFLRMKRPGEDKVRPACQHKPRR-
                                                                                                               IYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                    KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYO
                                                                                                                                                                                          TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
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                                                                                                                                                                                                                                                                   534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACH7_HUMAN STANDARD; PRT; 502 AA.
95544, 018262; 096RH2; 099555, 09BXH0;
01-JUNY-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
8-FFB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
CHRNA7 OR NACHRA7.
                                                                                            85;
        (POTENTIAL) (POTENTIAL)
                         . .) (POTENTIAL)
                                                                          Length
                                                                                             119; Indels
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                                  -> F (IN REF. 2).
-> R (IN REF. 2).
00996E74EC7B9A56 CRC64;
                                                                          Score 1173.5; DB 1;
Pred. No. 1.2e-74;
       N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N -> F (IN REF. 2).
SIMILARITY)
                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed in Xenopus oocytes."; Mol. Pharmacol. 45:546-554(1994).
(BY
                                                                                             80;
                                                      56410 MW;
                                                                          29.0%;
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                                                       502 AA;
                                                                                  Similarity
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                                                                                            Matches 238;
        CARBOHYD
CARBOHYD
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SEQUENCE FROM N.A.
MEDIINE=97162233; PubMed=9009220;
Groot Kormelink P.J., Luyten W.H.M.L.;
Groot Kormelink P.J., Luyten W.H.M.L.;
"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAchR) subunits beta3 and beta4 and expression of seven nAchR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32.";
FEBS Lett. 400:309-314(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21818878; PubMed=11829490;
RRILEY B., Williamson M., Collier D.; Wilkie H., Makoff A.;
"A 3-Mb map of a large segmental duplication overlapping the alpha7-
nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
Genomics 79:197-209(2002).
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Proteomics 2:212-223(2002).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
SEQUENCE FROM N.A.
MEDLINE-97062879; PubMed=8906617;
MEDLINE-97062879; PubMed=8906617;
Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Breast cancer;
MEDLINE=21829512; PubMed=11840567;
MEDLINE=2.1829512; PubMed=11840567;
MEDLINE=2.1829512; PubMed=11840567;
Parris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A., Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
Zvelebil M.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Cloning and sequence of the human a7 nicotinic acetylcholine
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Heinemann S.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arredondo J., Grando S.A.; "Cloning cholinergic receptors in human keratinocytes."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Groot Kormelink P.J., Luyten W.H.M.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                       beta 4 subunits.";
J. Mol. Neurosci. 7:217-228(1996).
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STANDARD;
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P54131;
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                         GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; GO:000489; F:nicotinic acetylcholine-activated cation-se. .; GO:0000187; P:activation of MAPK; TAS. GO:0006832; P:small molecule transport; TAS.
         SUBCELLULAR LOCATION: Integral membrane protein.
MASS SPECTROMETRY: MW-54157.68; METHOD-MALDI.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02331; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_memb; 1.
Pfam; PF00252; NRTONCHANNEL.
TIGRRAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
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82; Mismatches 115; Indels
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D94B3A482EAA0E42 CRC64;
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A -> G (IN REF. 1 AND 7).
S -> N (IN REF. 2 AND 6).
S -> P (IN REF. 2 AND 6).
C -> S (IN REF. 8).
A -> G (IN REF. 1).
RWACS -> AWPAP (IN REF. 8).
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                               L25827; -; NOT_ANNOTATED_CDS. 223141; CAA80672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Multigene family.
SIGNAL 1 22. BY S
CHAIN 23 502 NEUR
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EMBL; AF885858; AAK68111.1; --
EMBL; L2527; -; NOT_ANNOTATED
EMBL; Z23141; CAA80672.1;
EMBL; AF32758; AAK19515.1; --
PIR; GO2259; GO2259
PIR; 137185; ACH0A7.
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                                                                                                                                          EMBL; X70297; CAA49778.1; -.
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                         -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC
TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                       GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                               534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
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"Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine chromaffin cells: molecular cloning, functional expression and allernafive splicing of the alpha 7 subunit.";

Eur. J. Neurosci. 7:647-655(1995).

-!- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRARES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-72003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
TISSUE-Addreanl medulla,
MEDILINE-95346009; Pubmed-7620615;
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms=2;
Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P54131-2; Sequence=VSP_000075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P54131-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVV 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 VEMSAVAGPPATNGNLLYI--GFRGLDTMHCAP-TP---------DSGVVC 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGGDISSYVLNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIASMALLGFTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYHHHDPDGGKMPKWTRVVLLNWCAWFLRMKRPG-----EDKVRPACQHNERRCS--LAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628 VELKE-RSSKSLLANVLDIDDDFR----HNCRPMTPGGTLPHNPAFYRTVYGQGDDGSI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                           NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74;
                                                                                                                    InterPro: IRR006202; Neur_channel_memb.
InterPro: IRR006202; Neur_channel_memb.
InterPro: IRR006202; Neur_channel.
InterPro: IRR006201; Neur_channel.
Pfam; PF02931; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
IGRFAM9; ITGR00860; LIC; 1.
PROSITE: PS00236; NEURCTE.ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Iransmembrane; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (in isoform Short).
P_000075.
                                                                                                                                                                                                                                                                                         ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEE5D0B3820D42D5 CRC64;
                                                                                                                                                                                                                                                                                                                                            POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%; Score 1157; DB 1; 46.4%; Pred. No. 1.7e-73; iive 76; Mismatches 122;
                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing
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                                                                                                         EMBL; X93604; CAA63802.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.44
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                      487
161
210
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CARBOHYD
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                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                             Ballivet M., Alliod C., Bertrand S., Bertrand D.; "Nicotinic acetylcholine receptors in the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                     -i - FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
-i - SUBCELLULAR LOCATION: Integral membrane protein.
-i - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R PRIX; 568284; 568289.
R PRIX; 568288; 568289.
R HSSP, P58154; 119B.
R WormPep; F2566.3; CE09639.
R InterPro; IPR006029; Neu_channel_memb.
R InterPro; IPR006202; Neur_chan_LBD.
R InterPro; IPR006202; Neur_chan_LBD.
R Pfam; PF02931; Neur_chan_LBD; 1.
R Pfam; PF02932; Neur_chan_memb; 1.
R PRINTS; PR00252; NRUNCHANNEL; 1.
R PRINTS; PS00256; NEURCHANNEL; 1.
R PROSITE; PS00256; NEURCHANNEL; 1.
R RECEPLOT; POSISYBACHIC membrane; Ionic channel; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTEWTIAL).

N-LINKED (GLCNAC. .) (POTEWTIAL).
                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bristol N2;
Nelson J., Wohldmann P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA-TYPE CHAIN.
EXTRACELLULAR (POTENTIAL)
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                                                                                                498 AA
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 DRLCLIIFTMFAILATIAVLLSAPHII 768
              POTENTIAL.
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                                                                                                  PRT;
                                                                                                                                                                                                                                                                                 STRAIN-Bristol N2;
MEDLINE-96196478; PubMed-8627624;
                                                                                                                                                                                                                                                                                                                                                    Mol. Biol. 258:261-269(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X83887; CAA58764.1; -.
                                                                                                  STANDARD;
                                                                                                                                                                                                Caenorhabditis elegans.
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498
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252
279
314
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93
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=6239;
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231
261
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147
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93
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P48180;
742
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CARBOHYD
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                                                                                                                                               NOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT 414
                                                                                                                                                                                                          NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG 474
                                                                                                        304 TASTVFTVYVLNLHYRTPETHDMGPWTRNLLLYWIPWILRWKRPGHN--LTYASLPSLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSERKHQILSDVELKERSSKSLLANVLD-----IDDDFRHNCRPMTPGGTLPHNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
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                                                                                       295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
                                                         Gaps
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bossy B., Ballivet M., Spierer P., "Conservation of neural nicotinic acetylcholine receptors from Drosophila to vertebrate central nervous systems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha-like chain 1 precursor.
NACR-ALPHA-96AA OR ACRB OR ALS OR ACR96AA OR CG5610.
Drosophila melanogaster (Fruit fly).
EUKARYOGE; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Weoptera; Endopterygota; Diptera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                             Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     725 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.3%; Score 1104; DB 1; Length 4 43.3%; Pred. No. 8.6e-70; Live 76; Mismatches 139; Indels
57169 MW; E463ABB40AC9FA82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567 AA.
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MEDLINE=88283626; PubMed=2840281;
                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. 7:611-618(1988).
498 AA;
                                          Best Local Similarity
Matches 227; Conserv
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                            Query Match
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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Bennos P.V., Barman B.P., Bhandari D., Bolshakov S.,
RA Benson K.Y., Bennos D.V., Barman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pluck J.,
RA Harris N.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Alash P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Alali M., Kalush F., Karpen G. G.H., Ke Z., Kenlson J.A., Kalush E.,
Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Kimmel B.E., McIntosh T.C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remindton K., Saunders R., Pecleb J.M.,
RA Reinert K., Remindton K., Saunders R., Perlet K., Smith T.,
Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
Shue B.C., Siden-Kiamos I., Sinpson M., Strong R., Sun E.,
RA Willams S.M., Woodage T., Wonley K.C., Wu D., Yang S., Yao Q.A.,
RA Wallsams S.M., Woodage T., Wonley K.C., Wu D., Yang S., Yao Q.A.,
RA Hang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Rang Y.-J. Yeh R.-Z., Zaveri J.S., Zhan M., Zhong S., Zhu X., Smith H.O.,
RA Jabeng X.H., Zhong F.N., Zhong W., Venter J.C.;
RY Sheng S.A., Myers E.W., Rubin G.D.ON,
RY Sheng S.A., Myers E.W., Rubin G.D.ON,
RY Sheng S.A., Myers E.W., Rubin G.M., Sheng S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLUIAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: CNS IN EMBRYOS.
-1- DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR LARVAE STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEORGE BIOL 3: RESEARCHO083.1-RESEARCH0083.22(2002).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement ({ or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S00381; ACFFA1.
Flybasę; Fbgn0000036; nAcR-alpha-96Aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Berkeley;
MEDLINE-22426069; PubMed-12537572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       systematic review.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------EEPEEDQPPEVLTDVYHLPP-----DVDKFVNYDSKRFSGDYGIP 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 ALPASHRFDLAAAGGISAHCFAEPPLPSSLPLPGADDDLFSPSGLNGDISPGCCPAAAAA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----WIRIVFLCWLPWILRMSRPGRPL 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 YTVNLIIPCVGISFLSVLVFYLPSDSGEKISLCISILLSLTVFFLLLAEIIPPTSLTVPL
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_memb; 1.
PRINTS: PR00522; Neur_chan_memb; 1.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                   -QLQD----ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                                                                                                                                                 291 SWIFLLIYLNLS-AKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLÓLSFGLTLMQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVDEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 GTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605 ILEFPTTPCSDTSSERKHQILSDV-ELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLP
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                                                                                                                         RECEPTOR PROTEIN, ALPHA-
                                                                                                                                                                                                                                             ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                              ; Score 888; DB 1; Length 567;
; Pred. No. 1.3e-54;
91; Mismatches 168; Indels 102;
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08E1F721FB2A92AC CRC64;
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N-LINKED (GLCN)
                                                                                                                          ACETYLCHOLINE
                                                                                                                                    LIKE CHAIN 1.
EXTRACELLULAR
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538
108
567 AA;
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DISULFID
DISULFID
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VARIANT
CONFLICT
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TRANSMEM
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516 AA.

PRT;

STANDARD;

ACH1_MANSE ID ACH1_MANSE

RESULT 8

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                  Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRTONCHANNEL.
TIGRFAMS; TIGRO0860; LIC; LIC; LIC; PR0371E; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUT. J. NEULOSCI. 10:879-889(1998).

EUT. J. NEULOSCI. 10:879-889(1998).

EUT. J. NEULOSCI. 10:879-889(1998).

EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain precursor (MARAI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                         Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P., Reynolds S.E., Wolstenholme A.J., Wonnacott S., "Characterization of a nicotinic acetylcholine receptor from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASSOCIATED WITH RECEPTOR ACTIVATION
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N-LIKKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LIKED (GLCNAC. .) (POTENTIAL).

E7A71E8C45D13BD2 CRC64;
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36.6%; Pred. No. 1.5e-54;
ive 65; Mismatches 141; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIKE CHAIN.
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98424077; PubMed-9753155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Postsynaptic membrane,
Transmembrane; Multigene family
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132
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516 AA;
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Matches 199; Conserv
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SEQUENCE
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InterPro; IPR006202;
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                  NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
                                   ------DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNL
                                                                                                            ----WIRIVFLCWLPWILRMSRPGRPLILEFP
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                                                                                                                                                            IIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL----
                                                                                                                                                                                                                                                                   308 LFTMILDTFSICVTVVVLNVHFRSPQTHTMSPWVRRVFIHVLPRLLVMRRP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91092263; PubMed-1702381;
Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
Darilson M.G., Sattelle D.B., Barnard B.A.;
Sequence and functional expression of a single alpha subunit of an
insect nicotinic acetylcholine receptor.";
EMBO J. 9:4391-4398(1990).

-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-007-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acctylcholine receptor protein, alpha-Ll chain precursor.
Schistocerca gregaria (Desert locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
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InterPro; IPR006029; Neu_channel_memb.
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-----adlaskrilrhahnsklsaaaaaaaaaasssaasspdsirhhilhqhqhqhhi
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                                  FIGHT, Frossi, Neul_Chanler, 1.
PIGHTS; PROSS; NICHANNEL.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 EKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    608 FPTTPCSDTSSERKHQILSDVELKERSSKSLLA----NVLDIDDDFRHN-----
                                                                                                                      ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                                                                                                    Length 557;
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                                                                                                                                                                                                                                                                                                                                                                  Score 873; DB 1;
Pred. No. 1.4e-53;
                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC.
ALA/SER-RICH.
HIS-RICH.
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IPR006201; Neur_channel.
           Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                       Transmembrane; Multigene family SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                             90;
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ID ACH2_HUMAN STANDARD;
AC 01582; 09HAQ3;
DT 01-NOV-1997 (Rel. 35, Created)
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36.8%;
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557 AA;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Blechschmidt K., Rosenthal A.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                  TISSUE-Hypothalamus;
MEDLINE-97062879; PubWed-8906617;
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
beta 4 subunits.";
J. Mol. Neurosci. 7:217-228(1996).
                                                                                               Euteleostomi;
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 118502; -.

GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan.
GO; GO:0004899; F:nicotinic acetylcholine-activated cation-se.
GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0007268; P:synaptic transmission; TAS.
InterPro; IPR0066029; Neu_channel_memb.
InterPro; IPR006201; Neu_channel_memb.
InterPro; IPR006201; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_memb; 1.
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Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                          Groot Kormelink P.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR.
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EMBL; Y16281; CAA76154.1; -.
EMBL; AF311103; -; NOT_ANNOTATED_CDS.
GGNEW; HONC:1956; CHRNA2.
MIM; 118502; -.
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TIGREAMS; TIGR00860; LIC; 1.
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289
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                                                                            Homo sapiens (Human)
                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                  486 ELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIASMALLGFTLPP
                                                                                                                                                                                                                                                                                                                                                                       292 DCGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629 ELKERSSKSLLANVLDIDDDFRHNCR-PMTPG-GTLPHNPAFYRTVYGQGDDGSIGPIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    687 TRMPDA---VTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 GYH---EKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 VHHRSPSTHTMPHWVRGALLGCVPRWLLMNRPPPPVEL---CHPLRLKLSPSYHWLESNV
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                                                                                                                                                          Gaps
BY SIMILARITY.

ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

A -> T (IN REF. 3). .) (POTENTIAL).

MW; 7F512B06CCD9AAFD CRC64;
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P32297; Q15823; Q96RH3; Q99553; Q9BQ93;
01-OCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
                                                                                                                                                         75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fornasari D., Chini B., Tarroni P., Clementi F.; "Molecular cloning of human neuronal nicotinic receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                Length
                                                                                                                                                          Indels
                                                                                                                              21.0%; Score 848.5; DB 1; 36.7%; Pred. No. 6.6e-52;
                                                                                                                                                          Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                546 DSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL----
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                                         79 N-
129 N-
235 N-
125 A
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Best Local Similarity 36.7
Matches 183; Conservative
                                          79
129
235
125
529 AA;
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rachiguez A.C., Gilmwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).

MEDILINE-9716233; PubMed-9009220.

Groot Kormelink P.J. Luyten W.H.M.L.;

"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32.";
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99118870; PubMed-9921897; Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.; "The Structures of the human neuronal nicotinic acetylcholine receptor bera2- and alpha3-subunit genes (CHRNB2 and CHRNA3)."; Hum. Genet. 103:645-653(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L., "Characterization of the human beta4 nAChR gene and polymorphisms in CHRNA3 and CHRNA4.";
             Mihovilovic M., Roses A.D.; "Expression of mRNAs in human thymus coding for the alpha 3 subunit of a neuronal acetylcholine receptor."; Exp. Neurol. 111:175-180(1991).
                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).

MEDLINE-97062879; PubMed-8906677;

Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,

Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;

"Comparative structure of human neuronal alpha 2-alpha 7 and beta
"Comparative actylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arredondo J., Grando S.A.; "Cloning cholinergic receptors in human keratinocytes."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anand R., Lindstrom J.;
Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            numan and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANT LEU-21 INS.
MEDLINE-21342809; PubMed=11450844;
                                                                                                                                                                                                     Mol. Neurosci. 7:217-228(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932;
 MEDLINE-91114756; PubMed-1989896;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                       Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.

SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).

SUBUNITS: ALPHA AND NON-ALPHA (BETA).

ALTERNATIVE PRODUCTS:

EVENT. SUBUNITS: ALPHA AND SUBURDANE PROTECTION.

EVENT. SUBUNITS: ALPHA AND NON-ALPHA (BETA).

SUBUNITS: ALPHA AND NON-ALPHA (BETA).

SUBUNITS: ALPHA AND NON-ALPHA (BETA).

SUBUNITS: ALPHA AND SUBURDANE.

SUBUNITS: ALPHA AND SUBURDANE.

SUBUNITS: ALPHA AND SUBURDANE.

NON-ALPHA (BETA).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
MALAV -> MGSGPL (in isoform 2).
/FIId=VSP_000073.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                   IsoId=P32297-1; Sequence=Displayed;
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EMBL, M303031, AAB40110.1;
EMBL, V08418, CAA69695.1;
EMBL, AJ007783, CAA07682.1;
EMBL, AJ007784; CAA07682.1;
EMBL, AJ007785; CAA07682.1;
EMBL, AJ007785; CAA07682.1;
EMBL, AJ007785; CAA07682.1;
EMBL, AJ007785; CAA07682.1;
EMBL, BC001542; AAH01642.1;
EMBL, BC0002996, AAH01642.1;
EMBL, BC000213; AAH00513.1;
EMBL, AJ00788584; AAK68110.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M86383; AAC84176.1; -.
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170
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PIR; A53956; A53956.
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LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK 354
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                                                                                                                                                                                                                                                                                                                             415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
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                                                                                                                                                                               Gaps
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                                 -> ALAAPGAVA (IN REF. 2).
                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACH2_DROME STANDARD; PRT; 576 AA.
P17644; Q9VC73;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain 2 precursor.
NACR-ALPHA-96AB OR ACRE OR SAD OR ACR96AB OR CG6844.
Drosophila melanogaster (Fruit fly).
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                                                                                                                                                  DB 1; Length 503;
                                                                                                                                                                ; Pred. No. 1.1e-51;
97; Mismatches 166; Indels
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Ephydroidea; Drosophilidae; Drosophila
                                         LSPP -> CRA (IN REF. 1).
D -> G (IN REF. 1).
DD -> TT (IN REF. 1).
I -> S (IN REF. 1).
L -> V (IN REF. 1).
L -> V (IN REF. 1).
H, 8A9EBC5D71AEC7D6 CRC64;
                FTIG=VAR_013240
                                                                                                                                                   Score 845;
                                 VSLPLALSP
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                                                                                                                      57309 MW;
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35.2%;
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Matches 178; Conservative
                                                                                                                      503 AA;
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	OY 654 RPMTPGGTLPHNPAFYRTVYGQGD	Qy 747 IIFTWFAILATIAVLLSAPH1 767 : :::: : Db 530 WLFWIASLVGTFVILGEAPSL 550	SULT 13 H3_DROME ACH3_DRO			OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila. OX NCBT TaxID=7227:		RT "Primary structure of a developmentally regulated nicotinic RT acetylcholine receptor protein from Drosophila."; RE EMBO J. 5:1503-1508(1986).	5. 2 5. 5 6.,		RA Wadsworth S.C., Kosenthai L.S., Kammermeyer K.L., Fotter M.B., RA Nelson D.J.; RT "Expression of a Drosophila melanogaster acetylcholine receptor- RT related gene in the central nervous system.";		RX MEDLINE=20196006; PubMed=10731133; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	RA Sutton G.G., Wortuman J.K., rangell m.D., Jinding V., Chen L.A., RA Brandon R.C., Rogers YH.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An HJ., Andrews-Pfannkoch C., Baldwin D.,	RA Ballew K.M., Basu A., Baxendale J., Bayraktarogiu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	A Cherry J.M., Cawley S., Danke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,	KA FOSIEF C., Gabriellan A.E., Garg N.S., Gelodru W.M., Glassei n., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
	5 1 5 4	3	4 K H I	, <u>, , , , , , , , , , , , , , , , , , </u>			, 14, 14, 15, 1						ee per per per i		کابتاب <u>ہ</u>	man ann hain hain f	
-!- DEVELOPMENTAL STAGE: LATE EMBRYONIC A	CC This SWISS-PROT entry is copyright. It is produced through a collaboration cc between the Swiss institute of Bioinformatics and the EMBL outstation. CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).				PROSITE; PS00236; N Receptor; Postsynap Transmembrane; Mult	SIGNAL 1 21 CHAIN 22 576	DOMAIN 22 261 TRANSMEM 262 285 TRANSMEM 293 311	TRANSMEM 327 346 FOTEWILAL. DOMAIN 347 526 CYTOPLASMIC TRANSMEM 527 545 POTEWILAL. DISULEID 169 183 BY SIMILARYT DISTILEID 243 244 ASSOCIATED	CARBOHYD 65 65 CARBOHYD 254 254 CARBOHYD 570 570 SF0 SEQUENCE 576 AA; 65506 MW;	Query Match 20.9%; Score 843.5; DB 1; Length 576; Best Local Similarity 34.4%; Pred. No. 1.7e-51; Matches 193; Conservative 87; Mismatches 170; Indels 111; Gaps 11;	OY 290 HSWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLT 344	QY 345 LWQIIDVDEKNQLLYTNVWLKLEWNDMNLRWTSDYGGVKDLRIPPHRIWKPDVLMYNSA 404	QY 405 DEGFDGTYQTNUVVNNNGSCLYVPFGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464	Qy 465 DLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII 515	Oy 516 RRRILYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNWAETMPAT 575	OY 576 SDAVPL	Qy 599 RPGRPLILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNC 653

Db	530 WLFMIASLVGTFVILGEAPSL 550
RESULT ACH3_D	.T 13
A ID	ACH3_DROME STANDARD; PRT; 521 AA P04755: 09V2C3:
1	13-AUG-1987 (Rel. 05, Created)
E E	13-AUG-1987 (Rel. 05, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
DE	Acetylcholine receptor protein, beta-like chain 1 precursor.
SO So	NACK-BETA-04B OK ACKD OK AKD OK ACK04B OK CEL1348/CE12000. Drosophila melanogaster (Fruit fly).
88	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
28	Neoptera; Endopterygota; Diptera; Bracnycera; Muscomorpna; Ephydroidea; Drosophilidae; Drosophila.
X	NCBI_TaxID=7227;
R P P	[1] SEQUENCE FROM N.A.
RA	Hermans-Borgmeyer I., Zopf D., Ryseck RP., Hovemann B., Betz H.,
RT	Gundellinger B.D.; "Primary structure of a developmentally regulated nicotinic
RT.	<pre>acetylcholine receptor protein from Drosophila."; EMBO J. 5:1503-1508/1986).</pre>
RN	
RP PX	SEQUENCE FROM N.A. MPDTINE=88396843. Dubhad=3136037.
Z Z	ABOUTH E. Hermans-Boromever I., Betz H., Gundelfinger E.D.;
RT	"Characterization of an invertebrate nicotinic acetylcholine receptor
RT T	gene: the ard gene of Drosophila melanogaster."; FEBS 19++ 235:40-46/1088)
Z Z	[3]
RP	SEQUENCE FROM N.A.
K K	MEDLINE=661/4/20; Pubmed=2632/30; Wadsworth S.C., Rosenthal L.S., Kammermever K.L., Potter M.B.,
RA	Nelson D.J.;
E E	"Expression of a Drosophila melanogaster acetylcholine receptor-
R.	Mol. Cell. Biol. 8:778-785(1988).
RN I	[4]
ጸ 8 ማ ር	SEQUENCE FROM N.A.
RX.	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R R	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers YH.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Abril J.F., Agbayani A., An HJ., Andrews-Pfannkoch C., Baldwin D.,
RA Pa	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Reeson K V. Renos D V. Rerman R D. Rhandari D. Rolshakov S.
RA RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R A	cnerry J.m., cawley S., banike C., bavenport L.B., bavies F., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA RA	A Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleiscomann W., A Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

us-09-303-232-2.rsp

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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

A Jalai M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,

Jalai M., Kalush F., Karpen G.H., We Z., Kenhison J.A., Ketchum K.A.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Murphy J., Murphy D., Murphy D.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muray D.M., Nelson D.L.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Ran B.C., Siden Krämos I., Simpson M., Strong R., Sun E.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Science 297:1385-2195(2000).

C. :-FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

EERDS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLCHOLINE RECEPTOR PROTEIN, BETA-LIKE CHAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: CNS IN EMBRYOS.

DEVELOPMENTAL STAGES: LATE EMBRYON.C AND LATE PUPAL STAGES.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
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FF9BA2ABC0C3AA62 CRC64;
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PIR, S03012; ACFFNN.
FlyBase; FBgn0000038; nAcR-beta-64B.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_lbD.
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EMBL; X07956; CAA30778.1; --
EMBL; X07957; CAA30778.1; JOINED.
EMBL; X07958; CAA30778.1; JOINED.
EMBL; X070316; AAA28311.1; --
EMBL; AE003481; AAF47900.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ransmembrane; Multigene family
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323
481
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VARIANT
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Length 521;

Score 840; DB 1; Pred. No. 2.6e-51;

20.8%; 35.6%;

Local Similarity

Match

Query Best L

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6
                                 291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLOLSFGLTLMOIID 350
                                                                                                       410
                                                                                                                           469
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                                                                                                                                                                                                                                                                                                                                                                                                                                 365
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                                                      351 VDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
                                                                                                                                                                              411 TYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQL-Q
                                                                                                                                                                                                                                                                      306 TFIMNIVSILVTVIIINWNFRGPRTHRMPMYIRSIFLHYLPAFLFMKRPRKTRLRWMMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612 PCSDTSSERKHQILSDVELKERSS----KSLLANVLDIDDDFRHNC---RPMTPGGTLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKD
                                                                                                                                                                                                                                                                                                                        529 PCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.;
"Genes expressed in the brain define three distinct neuronal
nicotinic acetylcholine receptors.";
EMBO J. 7:595-601(1988).
-!- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN COMPORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    725 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHI 767
95; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THREE NON-ALPHA CHAINS.
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EFPTTPC-----SDTSSERKHQILSDVELKERSSKSLLANVL---DIDDDFRHN 652
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LISCLIVLVFYLPSDCGEKITLCISVLLSLIVFLLLITEIIPSTSLVIPLIGEYLLFTMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
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                                                                                                                                                                                                                                                                                                                                NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-2 CHAIN.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
E76C6360AP876336 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                                                                                                            PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.6e-51;
81; Mismatches 177; Indels
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                                                                                                                                                                     PIR; S00377; ACCH2N.
InterPro; IPR006029; New_chan_LBC.
InterPro; IPR006202; New_chan_LBC.
InterPro; IPR006201; New_chan_BC.
Pfam; PF02931; New_chan_LBD; 1.
Pfam; PF02932; New_chan_LBD; 1.
Pfam; PF02932; New_chan_memb; 1.
PRINTS; PR00252; NUNCONCHANNEL.
                                                                                          EMBL; X07340; CABS9645.1; JOINED.
EMBL; X07341; CABS9645.1; JOINED.
EMBL; X07342; CABS9645.1; JOINED.
EMBL; X07344; CABS9645.1; JOINED.
EMBL; X07344; CABS9645.1; JOINED.
EMBL; AJZ50360; CABS9625.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60675 MW;
                                                                               EMBL; X07339; CAB59645.1; -
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290
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520
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104
528 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                     467
653 CRPM---TPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGL 709
                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A., Ray N., Raftery M.A.; "Brain and muscle nicotinic acetylcholine receptors are different but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-87144271; PubMed-3821734;
Klarsfeld A., Daubas P., Bourachot B., Changeux J.-P.;
Klarsfeld A.; region of the chicken acetylcholine receptor alpha-
subunit gene confers tissue specificity and developmental control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA.
                                                                                                 DELTA, AND GAMMA CHAINS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE OF 180-227 AND 260-333 FROM N.A.
MEDLINE-84206570; PubMed-6327170;
Ballivet M., Nef P., Stalder R., Fulpius B.;
"Genomic sequences encoding the alpha-subunit of acetylcholine receptor are conserved in evolution.";
Cold Spring Harb. Symp. Quant. Biol. 48:83-87(1983).
                                                                              710 ILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.; "Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptors.";
                                       431 CERQAGKASGGPAPQVPLKGEEV---GSDQ-----GLTLSPSILR---
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MEDLINE=85270494; Pubmed=3860855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
MEDLINE-88283624; PubMed-3267226;
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EMBL; X07331; CAA30282.1; JOINED
EMBL; X12434; CAA30282.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression in transfected cells. Mol. Cell. Biol. 7:951-955(1987)
                                                                                                                                                                                                                                                            (Rel. 10, Created)
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SEQUENCE OF 1-12 FROM N.A.
                                                                                                                                                                                                                    STANDARD;
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293 IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVD 352
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InterPro; IPR006021; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan_LBD: 1.
Pfam; PF02932; Neur_chan_memb; 1.
Pfam; PF02922; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
PROSITE; PS00236; NEURONCHANNEL.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; POStsynaptic membrane; Ionic channel; Glycoprotein; Signal; Prosissmembrane.
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N-LINKED (GLCNAC. . ) (PROBABLE).
E -> D (IN REF. 4).
0B31B6EABD7B4D42 CRC64;
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EXTRACELLULAR
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X07335; CAA30282.1; JOINED. AJ250359; CAB59624.1; -. AF051909; AAC06012.1; -.
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52183 MW;
                                                                                                 M14808; AAA48565.1; -. M14809; AAA48564.1; -. IS0150; IS0150. S00376; ACCHAN.
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Search completed: August 13, 2003, 15:26:10 Job time: 19.1234 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 15:21:45; Search time 28.7606 Seconds (without alignments) 2574.698 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-303-232-2 4043 1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770

Scoring table:

283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB.seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	nicotinic acetylch	nicotinic acetylch	nicotinic receptor	alpha-bungarotoxin	nicotinic acetylch	alpha 7 neuronal n	nicotinic acetylch	hypothetical prote			9	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch			nicotinic acetylch	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch
SUMMARIES	a a		JN0113	T01378	JH0173	ACHUA7	G02259	868588	T25671	T19622	T19862	ACFFA1	S12359	A53956	ACFFA2	ACFFNN .	A37040	ACCH2N	A40110	ACCHAN	A24572	S60589	B37014	T09289	S12899	G02421	ACHUA1	ACBOA1	A28529	A24383
	DB	7	7	7	~ 1	٦	7	7	7	7	7	7	~	7	-	-	7	Н	7	-	7	~	~	7	7	7	П	П	ď	7
	Query Match Length		502	502	511	502	502	498	461	560	542	267	557	503	576	521	502	528	511	456	499	495	512	464	200	498	.457	457	457	457
ф	Query	29.2	29.5		28.9	28.7	28.6	27,3	25.0	24.4	24.0	22.0	21.6		20.9	20.8	20.8	20.7	20.5	20.5	20.4	20.3	20.3	20.5	19.9	•		19.8	19.7	19.6
	Score	1182.5	1179.5	1173.5	1168	1160.5	1155.5	1104	1009.5		968.5	889	873		843.5	841	840	838		827.5	824	820.5	820.5	8	806.5	802	802.5	0	٠	794
	Result No.	-	7	Э	4	2	9	7	ထ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

acetylcholine recenicotinic acetylch nicotinic acetylch nicotinic acetylch nicotinic acetylch acetylch nicotinic acetylch nicotinic acetylch protein P25366 4 [in nicotinic acetylch protein P25366 4 [in nicotinic acetylch n	nicotinic acetylch hypothetical prote
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792.5 789 789 787 783 782 779.5 779.5 779.5	773.5
	44

ALIGNMENTS

RESULT A57175	RESULT 1	
nic	otinic acet	nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
0 0 0 0	pecies: mu: ate: 05-Jar	C.becres: mus muscurus (mouse mouse) C.bate: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
C; Þ	ccession: / rr-Urtreger	57175 A.: Seldin, M.F.: Baldini, A.: Beaudet, A.L.
Gen	omics 26,	Genomics 26, 399-402, 1995
A; R	itle: Cloni eference nu	A;Title: cloning and mapping of the mouse alpha/-neuronal nicotinic acetylcholine rec A;Reference number: A57175; MUID:95324936; PMID:7601470
A; A	ccession: P	57175
A; W	A;Status: preliminary A;Molecule type: mRNA	IMINATY E: MRNA
A;R	A; Residues: 1-502 <orr></orr>	502 <orr></orr>
A; C	ross-refere	A;Cross-references: GB:L37663; NID:g790853; PIDN:AAC42053.1; PID:g790854
Š	eywords: br	ain; glycoprotein; lon channel; neurotransmitter receptor; phosphoprote
F;1	-23/Domain:	1-23/Domain: signal sequence #status predicted <sig></sig>
F F	4-502/Produ 31-254/Doma	<pre>ct: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr in: transmembrane #status predicted <tr1></tr1></pre>
F; 2	62-280/Doma	in: transmembrane #status predicted <tr2></tr2>
F;2	96-317/Doma	in: transmembrane #status predicted <tr3></tr3>
F, 7.	6,90,133/Bi	in: transmembrane #status predicted \int\ nding site: carbohydrate (Asn) (covalent) #status predicted
E :	65,413,427,	Binding site: phosphate (Ser) (covalent) #status predicted
F; 4	15/Binding 42/Binding	F;415/Ainding site: phosphate (Thr) (covalent) #status predicted F;442/Binding site: phosphate (Tyr) (covalent) #status predicted
Ō	uery Match	29.2%; Score 1182.5; DB 2; Length 502;
ÞΣ	atches 239	best Local Similatily 45.04; Figu. NO. 3.1677; Matches 239; Conservative 80; Mismatches 118; Indels 85; Gaps 10;
QY	297	- 13
qa	80	
QY	354	KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
qq	89	KNQVLTTNIWLQMSWIDHYLQWNMSEYPGVKNVRFPDGQIWKPDILLYNSADERFDATFH 127
Qy	414	TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
qq	128	THIST THE STATE OF
QY	474	GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533
qa	185	ADISSYIPNGEWDLMGIPGKRNEKFYECCKEPYPDVTYTVTWRRRTLYYGLNLLIPCVLI 244
δλ	534	
qa	245	SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 304
_		

Query Match 29.2%; Score 1179.5; DB 2; Length 502; Best Local Similarity 45.7%; Pred. No. 8.3e-77; 8.3e-77; Matches 237; Conservative 80; Mismatches 127; Indels 75; Gaps 9; 9; Qy 295 LLIYINLSAKVCLAGYHEKRLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV 351 ::: :: ::: :: ::: :: ::: :: ::: :: ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : :::: : :::: : :::: : :::: : ::::: : ::::::::::::::::::::::::::::::::::::	Qy 472 TGGDISSYVLNGEWELLGUYPGKRNEIYYRNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCV 531	Qy 730 IANDWKFAANVUDRLCLIFTMFAILATIAVLLSAPHII 768	Ouery Match 29.0%; Score 1173.5; DB 2; Length 502; Best Local Similarity 45.6%; Pred. No. 2.2e-76; Matches 238; Conservative 80; Mismatches 119; Indels 85; Gaps 10; predi Qy 297 IYLNLSAKVCLAGYHBKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 353
QY 582	Millar, velopmer	tter, J.M. Pptor promot PID:g65320 F.A.; Ray, N it but homol and is loca	80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3 51ine receptor 5protein; ion channel; neurotransmitter receptor; phosphopro- quence #status predicted <sig> inic acetylcholine receptor alpha-7 chain, neuronal #status nembrane #status predicted <tr1> nembrane #status predicted <tr2> nembrane #status predicted <tr3> nembrane #status predicted <tr3> nembrane #status predicted <tr4> s: carbohydrate (Asn) (covalent) #status predicted phate (Tr) (covalent) #status predicted sphate (Tr) (covalent) #status predicted sphate (Tr) (covalent) #status predicted</tr4></tr3></tr3></tr2></tr1></sig>

Page 3

		Db 187 DLQMLEADISNYISNGEWDLVGVPGKRNELYYECCKEPYPDVTYTITMRRRTLYYGL 243 Qy 525 NLIPCVLIASWALLGFTLPPDSGEKISLGVTILLSITVFLNMVAETWPATSDAVPL 581
Oy Dp	727 CNDIANDWKFAAMVVDRLCLIIFTWFAILATIAVLLSAPHII 768 :: : : : : : : :	RESULT 5 ACHUA7 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human N;Alternate names: cholinergic nicotinate receptor alpha-7 chain
RESULT JH0173 alpha-bu C; Specific C; Date: C; Access R; Schoel Neuron A; Title	bungarotoxin-binding protein alpha-2 chain precursor - chicken 16s: 31-101 gallus (chicken) 18sion: JH0173 19pi #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999 19pi #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999 19pi #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999 19pi #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999 19pi #sequence_revision protein cDNAs and Mabs reveal subtypes of this	C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999 C; Accession: 137185; A54194; S60309 R; Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J. MOI. Pharmacol. 45, 546-554, 1994 A; Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from thomers expressed in Xenopus occytes. A; Reference number: 137185; MUID:94195283; PMID:8145738 A; Accession: 137185 A; Status: translated from GB/EMBL/DDBJ
A; Rest A; Acce A; Rest A; Cros A; Expe A; Note	NA36544.1; PID:g63082	A; Residues: 1-502 cPENA A; Residues: 1-502 cPENA A; Residues: 1-502 cPENA A; Experimental source: brain neuroblastoma cell line SHSY-5Y R; Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S. Genomics 19, 379-381, 1994 A; Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotini
C; Supe C; Keyv F; 1-3(F; 31-E F; 239- F; 270- F; 304-	naptic pseudodend tus predicted <ae< td=""><td>A; Kerestore number: A34194; MULD: 9449214; FMID: 01002/U) A; Accession: A54194 A; Molecule type: mRNA A; Residuas: 24-363, 93, 365-374, A', 376-408, 'AWPAP', 414-502 CCHI> A; Residuas: 24-363, 93, 365-374, A', 773736; PIDN: CAA80672.1; PID: 9457737 A; Experimental source: retina C; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localii A; Genetics: A; Genetics:</td></ae<>	A; Kerestore number: A34194; MULD: 9449214; FMID: 01002/U) A; Accession: A54194 A; Molecule type: mRNA A; Residuas: 24-363, 93, 365-374, A', 376-408, 'AWPAP', 414-502 CCHI> A; Residuas: 24-363, 93, 365-374, A', 773736; PIDN: CAA80672.1; PID: 9457737 A; Experimental source: retina C; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localii A; Genetics: A; Genetics:
F;54/I Quer Best Matc	#status predicted 2; Length 511; 16; Indels 100; Gaps 12;	A;Cross-references: GDB:138751; OMIM:118511 A;Map position: 15q14-15q14 A;Note: defects in this gene have been associated with mental retardation and schizop C;Complex: the functional receptor molecule is a heteropentamer with two alpha chains C;Superfamily: acetylcholine receptor
oy Dp	285 NGLNKHSWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLT 344 : : :	C.Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter recept. F;1-23/Domain: signal sequence #status predicted <sig> F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr F;24-502/Product: transmembrane #status predicted <tri> F;21-254/Domain: transmembrane #status predicted <tri></tri></tri></sig>
Oy Db	345 LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA 404 :	F;262-380/Jonain: Liaismembrane #status predicted <1737 F;206-317/Domain: transmembrane #status predicted <1737 F;470-488/Domain: transmembrane #status predicted <1747 F;46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
Qy Db	405 DEGEDGTYQTNVVNRNNGSCLXVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464	F;150-164/Disullide bonds: #status predicted F;365,413/Binding site: phosphate (Ser) (covalent) #status predicted F;365,413/Binding site: phosphate (Thr) (covalent) #status predicted F;415/Binding site: phosphate (Thr) (covalent) #status predicted F;442/Binding site: phosphate (Tyr) (covalent) #status predicted
ογ	465 DLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFF 524	Query Match 28.7%; Score 1160.5; DB 1; Length 502; Best Local Similarity 45.1%; Pred. No. 1.9e-75;

us-09-303-232-2.rpr

Matches 237	?; Conservative 82; Mismatches 115; Indels 91; Gaps 12;	qa	185 ADISGYIPNGEMDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLI 244
Qy 297 Db 8	IXLNLSAKVCLAGYHEKRLIHDLIDPYNTLERPVINESDPLQLSFGLTLMQIIDVDE 353 : : :: :	. Oy Dp	534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581 :::
Qy 354 Db 68	KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413 	Qy	582
Oy 414 Db 128	THVVVRNNGSCLXVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473 [: : : :	Qy	613 CSDTSSERRHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAF 668
Oy 474 Db 185	GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533 	Qy	669 YRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRK 723
Qy 534 Db 245	ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581 :::	Qy	724 DDECNDIANDRKFAAMVVDRLCLIFFMFAILATIAVLLSAPHII 768 ::
Qy 582	GLSVVVTVIVLQXHHHDPDGGKMPKWTRVILLNWGMFLRMKRPGEDKVRP-ACQHKQRR 363	RESULT S68588	7
QY 613 Db 364	CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPWTPGGTLPHNPAF 668	C; Spec	ext_change 20-Aug-1
Oy 669 Db 402	669 YRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRK 723	K; Ball J. Mol A; Titl A; Refe	179c, M.; Allion, C.; Bertrand, S.; Bertrand, D. Biol. 258, 261-269, 1996 e: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans. Enter a mumber: 568587; MUID:96196478; PMID:8627624
Qy 724 Db 450	724 DDECNDIANDWKFAAMVVDRLCLIIFTWFAILATIAVLLSAPHII 768 ::	A; Acce A; Stat A; Mole A; Resi	ission: Socoso Lus: nucleic acid sequence not shown coule type: mRNA dues: 1-498 GBALD
RESULT 6 G02259 alpha 7 neuron	nal nicotinic acetylcholine receptor - human	A; Cros C; Supe C; Keyw F; 1-19 F; 20-4	A;Cross-reterences: EMBL:Absob; NID:90/2007; FIDN:CANDOTOW.1; FID:90/2000 C;Superfamily: acetylcholine receptor C;Reywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra F;1-19/Domain: signal sequence #status predicted <sig> F;20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <m< td=""></m<></sig>
C;Species: Hor C;Date: 21-Dec C;Accession: (R;Leonard, S.	no sapiens (man) c-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999 302259	Query Ma Best Loc Matches	y Match 27.3%; Score 1104; DB 2; Length 498; Local Similarity 43.3%; Pred. No: 2.1e-71; hes 227; Conservative 76; Mismatches 139; Indels 82; Gaps 8;
submitted to A; Reference nu A; Accession: (A; Status: prel	submitted to the EMBL Data Library, November 1995 A.Reference number: H00936 A.Accession: G02259 A.Status: preliminary, translated from GB/EMBL/DDBJ	QY Db	295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK 354
A; Molecule tyl A; Residues: 1 A; Cross-refer C; Superfamily:	MOLECULE type: mRNA Residues: 1-502 <led3 (led5)<br="">Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077 Superfamily: acetylcholine receptor</led3>	QY Db	355 NOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT 414 ::
Query Match Best Local Similarity Matches 237; Conser	28.6%; Score 1155.5; DB 2; Length 502; Similarity 45.1%; Pred. No. 4.4e-75; 7; Conservative 80; Mismatches 117; Indels 91; Gaps 12;	Qy	415 NVVVRNNGSCLYVPPGIFKSTCKIDITWPPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG 474 :: : : : :
Qy 297 Db 8	IYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPYLNESDPLQLSFGLTLMQIIDVDE 353 :: :	QY	475 -DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533 : : : : :
Oy 354 Db 68	KNQLLVTNVWLKLEWNDMNLRMNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413 : : : : : :	. qa	534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581
Oy 414 Db 128	INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMRFGSWTYDGFQLDLQLQDETG 473 :	QY	582
Qy 474	GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533	Ολ	617 SSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNP 666 : : : : : : : :

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Db 454 DKEEQACNNWKFAAMVVDRLCLYVFTIFILVSTIGIFWSAPYLV RESULT 8 RESULT 8 Hypothetical protein D2092.3 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_cf C:Accession: 725671 R:Gattung, S.; Maggi, L. submitted to the EMBL Data Library, February 1997 A:Description: The sequence of C. elegans cosmid D2092.	A Accession: 725671 A Accession: 72571 A Accession:
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13;
                                                                                                                                                                                                                                                                                                                                      SCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDET 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SDVELKERSSKSL 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RQYLIEVERHILTRPNGNGHSAVDKAVHLDLSTGNPHSDAKKSSPSPKRT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----IDDDF-RHNC----RPMTPG-GTLPH-----NPAFYRTVYG 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTTOMNGALDSSINKYTCTKVTRPLENGSATINHKSSPQINPINNNIYK 484
                                                                                                                                                         :293778; PIDN:CAB07843.1; GSPDB:GN00019; CESP:C31H5.3 lone C31H5
                          uence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OC9.2 - Caenorhabditis elegans
is elegans
quence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                            24.4%; Score 988; DB 2; Length 560;
37.2%; Pred. No. 5.3e-63;
ative 85; Mismatches 152; Indels 124; Gaps
                                                                                                                                                                                                                                 39/2; 270/1; 299/1; 336/3; 372/2; 456/3
line receptor
H5.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLIFTMFAILATIAVLLSAPHIIV 769
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                                                                                                                 ranslated from GB/EMBL/DDBJ
                                                                    ta Library, April 1997
53
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A/Gene: FlyBase:nAcR-alpha-96Aa
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A/Cross-references: FlyBase:FBgn000036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDL--- 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 VTIMTKAILHHTGKVVWKPPAIYKSFCEIDVEYFPFDEQTCFMKFGSWTYDGYMVDLRHL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:::|::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::|:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 SWIFLLIYLNLS-AKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 DVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 ILEFPTTPCSDTSSERKHQILSDV-ELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLP
A:Cross-references: EMBL:X07194; NID:97575; PIDN:CAA30172.1; PID:97576 A:Note: 538-Tyr was also found C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.0%; Score 889; DB 1; Length 567
35.2%; Pred. No. 6.7e-56;
.ive 91; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MFAILATIAVLLSAPHI 767
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Matches 196; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: X
A;Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1;
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRILYYFFNLIIPCVLIASMALLGFT 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 EKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWLKLEWNDM 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQ-----DETGGDISSYVLN 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKHQILSDVELKE------RSSKSLLANV-----LDIDDDF--RHN-CRPM 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 APSEMTP-----RVTY-----SKVWAESYVEDVVWTELNKYMQKACLELKNI 483
                                                                                                              A; Accession: T19862
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-542 <WIL>
A; Resire references: EMBL: Z70266; PIDN: CAA94206.1; GSPDB:GN00028; CESP: C40C9.2
A; Experimental source: clone C40C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FYRLLADLRHNYDPYERPVANASEPLVVSVKIYLQQILDVDEKNQVITLVAMIEYQWTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 NLRWNTSDYGGVKDLRIP--PHRIWKPDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPP
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A; Ablecule type: DNA
A; Residues: 1-57 C BOS>
A; Residues: 1-57 C BOS>
A; Cross-references: GB:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-56 C BOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 968.5; DB 2;
Pred. No. 1.3e-61;
9; Mismatches 144;
                                           Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.0%; Scor
38.7%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 208; Conservative
R;Hembry, C.
submitted to the EMBL Data
A;Reference number: Z19188
A;Accession: T19862
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sequence of the mature human nicotinic acetylcholine recept
                     submitted to the EMBL Data Library, June 1990
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                                                       A; Description: Nucleotide s
A; Reference number: S21338
A; Accession: S21338
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Best Local Simi
Matches 178;
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A; Title: Sequence and functional expression of a single alpha subunit of an insect nicot A; Reference number: $12359; MUD:91092263; PMID:1702381
A; Accession: $12359
A; Accession: $12359
A; Accession: $12359
A; Molecule type: mRNA
A; Residues: 1-57, CAMRA
A; Residues: 1
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C;Date: O'Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C;Accession: A55956; S21338
R;Mihovilovic, M.; Roses, A.D.
R;Mihovilovic, M.; Roses, A.D.
A;Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal A;Reference number: A53956 MUD:91114756; PMID:1989896
A;Accession: A53956
A;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --CRPMIPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLI 710
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Matches 197; Conservative
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A; Residues: 1-503 <MIH>
A; Cross-references: GB:M37
R; Anand, R.; Lindstrom, J.
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nicotinic acetylcholine receptor alpha-2 chain precursor - fruit fly (Drosophila mela
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EMBO J. 9, 2671-2677, 1990
A;Title: Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD, a novel
A;Reference number: S11679; MUD:90360975; PMID:1697262
A;Accession: S11679
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jun-2002
C;Accession: S11679; S10306; S11084
                                                                                                                                                                                                                                                                                                                                                                                         NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
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                                                                                                                                                                                                                                                                                                               Gaps
A; Molecule Lype: mRNA
A; Residues: 30-503 < ANN>
A; Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C; Genetics:
A; Gene: GDB:CHRNA3
A; Cross-references: GDB:125219; OMIM:118503
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A,Residues: 1-576 <SBA:
A,Cross-references: BMBL:X53583; NID:g8532; PIDN:CAA37652.1; PID:g8533
A,Note: 232-11e was also found
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                                                                                                                                                                                                                                                             Length 503;
                                                                                                                                                                                                                                                        20.9%; Score 845; DB 2; L
35.2%; Pred. No. 8.2e-53;
iive 97; Mismatches 166;
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Nucleic Acids Res. 18, 3640, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMVVDRLCLIIFTMFAILATIAVLL 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 15924-15924
C; Superfamily: acetylcholine receptor
C; Keywords: neurotransmitter receptor
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                                                                                                                                                                                                                                                                                                                                                                                                       A;Genet: FlyBase:nAcR-alpha-96Ab
A;Cross-references: FlyBase:FBgn000039
A;Cross-references: FlyBase:FBgn000039
A;Map position: 38 96A
A:Introns: 84/3; 136/2; 196/3; 250/1; 445/2; 512/3
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
C;Keywords: glycoprotein; acetylcholine receptor alpha-2 chain #status predicted <SIG>F;42-250/Domain: stranelular #status predicted <SIG>F;42-260/Domain: transmembrane #status predicted <TM>>
F;20-291/Domain: intransmembrane #status predicted <TM>>
F;31-349-256/Domain: intransmembrane #status predicted <TM>>
F;32-345/Domain: intransmembrane #status predicted <IM>>
F;52-445/Domain: transmembrane #status predicted <IM>>
F;52-245/Domain: transmembrane #status predicted <IM>>
F;65,254,570/Aliding site: carbohydrate (Asn) (covalent) #status predicted
F;169-183/Disulfide bonds: #status predicted
A;Title: Sequence of D-alpha-2, a novel alpha-like subunit of Drosophila nicotinic acety
A;Reference number: S10306; MUID:90301489; PMID:2114015
A;Accession: S10306
                                                                                                                                                                                                                          A;Title: Structure and developmental expression of the D-alpha-2 gene encoding a novel A;Reference number: S11084; MUID:90353591; PMID:2117557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 HSW-----IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 DEGFDGTYQINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DL----QLQD-----ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---WIRIVFLCWLPWILRMS 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 SLALPLIGKYLLFTMLLVGLSVVITIIILNIHYRKPSTHKMRPWIRSFFIKRLPKLLLMR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            599 RPGRPLILEFPTTPCSDTSSERKHQILSDVELKE-----RSSKSLLANVLDIDDDFRHNC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 MQMNSGSSPDSLRRMQGRVGAGGCNGMHVTTATNRFSGLVGALGGGLSTLSGYNGLPSV 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 HIWRHCKPLCLLLVLLLLCETVQANPDAKRLYDDLLSNYNRLIRPVSNNTDTVLVKLGLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRRTLYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                 A;Cross-references: EMBL:X52274; NID:g7802; PIDN:CAA36517.1; PID:g7803 R;Jonas, P.; Baumann, A.; Merz, B.; Gundelfinger, E.D. FEBS Lett. 269, 264-268, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.9%; Score 843.5; DB 1;
Best Local Similarity 34.4%; Pred. No. 1.3e-52;
Matches 193; Conservative 87; Mismatches 170;
                                                                                                                                                                                                                                                                                                     A; Status: nucleic acid sequence not shown A; Molecule type: DNA A; Residues: 42-90, 'I', 92-576 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654 RPMTPGGTLPHNPAFYRTVYGQGD---
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                                                                                   A; Molecule type: mRNA
A; Residues: 1-576 <BAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 SDAVPL---
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                                                                                                                                                                                                                                                                                 A; Accession: S11084
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Cyteywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra (Fi24/Domain: signal sequence #status predicted <SIG> Fi25-234/Product: nicotinic acetylcholine receptor nonalpha chain #status, predicted <Fi>Fi25-236/Domain: extracellular #status predicted <EXT> Fi237-26/Domain: transmembrane #status predicted <TM1> Fi268-285/Domain: transmembrane #status predicted <TM2> Fi302-333/Domain: transmembrane #status predicted <TM3> Fi324-481/Domain: itransmembrane #status predicted <IM3> Fi324-481/Domain: transmembrane #status predicted <IM7> Fi382-500/Domain: transmembrane #status predicted <IM7> Fi482-500/Domain: transmembrane #status predicted <IM7> Fi482-500/Domain: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B.; Betz, H.; Gundelfinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nicotinic acetylcholine rec
nicotinic acetylcholine receptor nonalpha chain precursor – fruit fly (Drosophila mel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-72, V., 74-521 <HER>
A; Cross-references: EMBL: X04016; NID:97537; PIDN:CAA27641.1; PID:97538
A; Wadsworth, S.C.; Rosenthal, L.S.; Kammermeyer, K.L.; Potter, M.B.; Nelson, D.J.
Mol. Cell. Biol. 8, 778-785, 1988
A; Title: Expression of a Drosophila melanogaster acetylcholine receptor-related gene
A; Reference number: A28126; MUID:88174720; PMID:2832736
                                                                                                                                                                                                                                                gene:
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C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C; Accession: 503012; A38064; A26313; A28126; A38759
K; Sawruk, E.; Hermans-Borgmeyer, I.; Betz, H.; Gundelfinger, E.D.
FEBS Lett. 235, 40-46, 1988
A; Title: Characterization of an invertebrate nicotinic acetylcholine receptor
A; Reference number: 503012; MUID:88296842; PMID:3136037
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A; Residues: 1-521 <SAW>
A; Cross-references: EMBL:X07956; NID:g7602; PIDN:CAA30778.1; PID:g1065712
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A;Residues: 1-55,'G',57-72,'V',74-521 <SAW2>
R;Hermans-Borgmeyer, I.; Zopf, D.; Ryseck, R.P.; Hovemann,
EMBO J. 5, 1503-1508, 1986
A;Title: Primary structure of a developmentally regulated n
A;Reference number: A26313
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A;Introns: 22/1; 67/3; 119/2; 267/3; 467/3
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: FlyBase:FBgn0000038
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A,Residues: 1-521 <WAD>
A,Cross-references: BMBL:M20316
C,Genetics:
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187 NKNFVDLSDYWKSGTWDIIEVPAYLN-VYEGDSNHPTETDITFYIIIRRKTLFYTVNLIL 245	529 PCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATS 576	246 PTVLISFLCVLVFYLPAEAGEKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLF 305	dΩD	306 TFIMNTVSILVTVIIINWNFRGPRTHRMPMYIRSIFLHYLPAFLEMKFRFKTRLRWAMEM 365	612 PCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH 664	366 PGMSMPAHPHPSYGSPAELPKHISAIGGKQSKMEVMELSDLHHPNCKINRKVNSGGEL 423	NPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILK	424GCRRESESSDSILLSPEASKATEAVEFIAEHLRNE 462	725 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHI 767	463 DLYIQTREDWKYVAMVIDRLQLYIFFIVTTAGTVGILMDAPHI 505
187 N	529 P	246 P	- 222	306 T	612 P	366 P	665 N	424 -	725 p	463 D
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D. melanogaster ac
H. virescens acety
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Drosophila melanog
Drosophila melanog
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/SIDSI/gcgdata/geneseq/genesegp embl/AA2000.
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5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1107863 seqs, 158726573 residues
   GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries

    protein search, using sw model

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AAY50815
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Human neuronal nic Neuronal nicotinic

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AAY50816 ABB70382 AAW12368 ABB63683

1159.5 28.7 502 22 AABS2408
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acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, its requiatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (1) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster.
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                                  invention describes a novel nucleic acid (NA) encoding a nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                        LFRRIAASTIAFISYLGSFAAQLKNSSSSSSSSNSSNNSSTQILNGLNKHSWIFLLIYLN
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                                                                                                                                                                                                                                                                                                                                                   MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRHNQOLTTLQPRSLSTKH
                                                                                                                                                                                                                                                                                                                                                                                                                      HSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTQQPTNIRLCARKRQRLRRRRKRKPATPNETDIKKQQQLSMPPFKTRKSTDTYSTPAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLWIRIVFLCWLPWILRMSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIASMALLG
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                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                            Score 4043; 1
Pred. No. 0;
); Mismatches
 German.
                                                                                                                                                                                                                                                                                                                 ;
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26pp;
                                                                                                                                                                                                                                                                              100.0%;
100.0%;
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Matches 770; Conservative
                                                                                                                                                                                                                                               770 AA;
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 LEIYLNESAKVCLAGYHEKRELHDELDPYNTLERPVENESDPLQESFGLTLMQIIDVDEK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                     Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                           protein from clone Hva7-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Mismatches
                                                                                                                                                                                                                                                                                                                           Schulte T;
                                                                                            acetyl-choline receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1a; Page 17-19; 26pp; German
               Ř.
               AAY50815 standard; Protein;
                                                                                                                                                                                                                                            98DE-1019829
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                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361; Conservative
                                                                                                                                                                                                                                                                                                                                                      2000-014207/02.
                                                                                                                                                              Heliothis virescens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          496 AA;
                                                                                                                                                                                                                                                                                                  AG.
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                                                                                                                                                                                                                                                                                                                           Adamczewski M,
                                                                                                                                                                                                                                                                                                  (FARB ) BAYER
                                                                                               virescens
                                                                                                                                                                                                                                            04-MAY-1998;
                                                                 17-FEB-2000
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65
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                               LLALLPVSEQ ----GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEK
                                                                                                                                                                    DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRTLYYFFNLIIPCVLIA
                                                                                                                                                                                                                                       SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-------
                                                                                                                                                                                                                                                                                                        ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS
                                                                                                                                                                                                                                                                                                                                                                          SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG-----GTLPHNPAFYRTV
                                                                                                                                                                                                                                                                                                                                                                                           NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 37938; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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N-PSDB; ABL14485.
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ABB70382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransanission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                  412
                                                                                                                                                                      354
                                                                                                                                                  OGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDW 734
                                   317 SSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPPPP--
                                                                                                    295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
               ---WIRIVELCWLPWILRMSRPG---RPLILEFPTTPCS
                                                                                 DISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides {}^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                                                           virescens acety1-choline receptor protein from clone Hva7-2.
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                                                                                                                                                                                                                                     KFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIVS 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1a; Page 22-23; 26pp; German.
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Matches 319; Conservative
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Adamczewski M,

Sequence Query Match

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(FARB) BAYER

DE19819829-A1

17-FEB-2000

AAY50816;

AAY5081

04-MAY-1998; 04-MAY-1998;

11-NOV-1999

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28-SEP-1989;
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                                                                                                                                                                                                   9
                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
   invention
capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-interactions in higher eukaryotes for the development of insecticides, therapeutics of pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0176-ABL30511), and the encoded proteins
                                                                                                                                                                                           MKNAQLKLTEVDDDELWLAVRLAHCSSNISSSSTRTTSSNKRHNQQLTTLQPRSLSTKH
                                                                                                                                                                               1 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
                                                                                                                                                                                                                       HSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA
                                                                                                                                                                                                                                 181 TSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLHVLQVLLVSLQOWQLHVQQRSVL
                                                                                                                                                                                                                                                                                                                                                LFRRIAASTIAFISYLGSFAAQLKNSSSSSS-SSNSSNNSSTQILNGLNKHSWIFLLIYL
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                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
                                                                                                                                                            ä
                                                                                                                                      Length 327;
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 17841
                                                                                                                                       DB 22;
                                                                                                                                                 Pred. No. 4.4e-129;
                                                                                                                                                          4; Mismatches
                                                                                                                                       Score 1498.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB63683 standard; Protein; 311 AA.
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                                                                                                                                      37.18;
97.48;
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                          Matches 297; Conservative
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N-PSDB; ABL07786.
                                                     sequences (ABL01840 (ABB57737-ABB72072)
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                                                                                                                                                 Best Local Similarity
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NLSAK 305
                                                                                                                  327 AA;
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                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
  detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                          capable of detecting 1000 or more genes from brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                                                                                           invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
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                                                                                              Disclosure; SEQ ID NO 17841; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuronal alpha-bungarotoxin binding protein alphal subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                         discloses genomic DNA sequences (ABL16176-ABL30511), exsequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.8%; Score 1407.5; DB 2.88.6%; Pred. No. 9.7e-121; ive 18; Mismatches 12;
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New isolated nucleic acid
genes from Drosophila and
interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 88.6
Matches 257; Conservative
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alpha-bungarotoxin binding protein alpha 2; cholinergic;
                                              Weuronal alpha-bungarotoxin binding protein alpha2 subunit.
                                                                               ligand binding; ion channel
                        (first entry)
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N-PSDB; AAT59197.
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                                                                                                                                                                                                                                                                                                           Lindstrom JM,
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                       17-JUN-1997
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------CGRMTCSPTEEENLLHSGHPSEGDPDLAKILEEVRYIANRFRDQDEEEA 455
                                                                                                                                                     The alphal subunit (AAW1236B) and alpha2 subunit (AAW12369) amino acid sequences of chick neuronal alpha-bungarotoxin binding protein. (AABB) were deduced from newly isolated DNA molecules (AAF95196-97) obtd. from an 18-day chick embryo cDNA library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other activity of intact ABBP subtypes. The ABBP alphal and alpha2 subunits can also be used to produce subunit peptides for use as immunogens for used to pring antibodies to permit affinity purification of subtypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ADISGYISNGEWDLVGIPGKRTESFYECCKEPYPDITFTVTMRRTLYYGLNLLIPCV
                                                                                                                                                                                                                                                                                                                                                             295 LLIYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
                                                                                                                                                                                                                                                                                                                                                                           DEKNOLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 TGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFALIIRRRTLYYFFNLIIPCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTSSERKHQILSDVELKERSSKSLL-ANVLDIDDDFRH----NCRPMTPGGTLPHNPAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 QHKQRRCS--LSSMEMNIVSGQCSNGNMLYI--GFRGLDGVHCTPTTDSGVI-----
                                                                                    New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                     DB 18; Length 502;
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                                                                                                                                                                                                                                                                                                                  29.2%; Score 1179.5; DB 45.7%; Pred. No. 2.1e-99; tive 80; Mismatches 127
           STUDIES
                                                                                                                                    Example; Fig 2A-B; 18pp; English
                                                                                                                                                                                                                                                                       and their histological location
          (SALK ) SALK INST BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                         Conservative
                               Lindstrom JM, Schoepfer
                                                  WPI: 1997-118297/11
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                             502 AA;
                                                                N-PSDB; AAT59196
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standard; Protein; 511 AA.

AAW12369

AAW12369 ID AAW1 XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The alphal subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid sequences of Chick neuronal alpha-bungarotoxin binding protein (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97) obtd. from an 18-day chick embryo cDNA library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact ABBP subtypes. The ABBP alphal and alpha2 subunits can also be used to produce subunit peptides for use as immunogens for prepring antibodies to permit affinity purification of subtypes and their histological location.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
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/label= Sig_peptide
                                                                            31..511
/label= Mat_protein
Location/Qualifiers
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                                                                             387
                                                                                                       605 ILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH 664
                                                                                               NPAFYRTVYG-------QGDD--GSIGPIGSTRMPDAVTHHTCIKS--STEYELGLI 710
                                                                                                                                -WIRIVFLCWLPWILRMSRPG---RPL
                                                                                                                                                                                                                                                               Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit; brain tissue; screening; NAChR; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                                                                                                                                                                                                               Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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19. 25. 256
Tabel- TMD1
...te- "transmembrane domain"
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|abel=_TMD2
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/label= cytoplasmic_loop
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/label= TMD3
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N-PSDB; AAV12197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581
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                                                                                                                                                                                                                                                                                                                                                                    compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 IYLNLSAK---VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.7%; Score 1159.5; DB 15;
45.1%; Pred. No. 1.4e-97;
tive 82; Mismatches 115; I
Page 80-81; 99pp; English.
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237; Conserv
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those characterised by overexpression and/or activation of the amplified antibodies. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. Asc5842t to AAC5836 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58357 to AAC58357 to AAB24089 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO8099, PRO880, PRO880, PRO8481, PRO943, PRO1009, PRO1025, PRO1009, PRO1025, PRO1009, PRO1005, PRO1009, PRO1187, PRO1281, PRO23, PRO39, PRO8141, PRO1181, PRO1281, PRO2188, PRO antagonists can be used to inhibit tumour cell proveth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO polynucleotides encoding PRO polypeptides, useful in ent, diagnosis and prevention of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment,
                                                                                                                                    AAB24088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-1
                                                             RESULT 10
                                                                              AAB24088
                                                                                                                                    473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 IYLNLSAK----VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLJAQYFASTMIIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-7 subunit bNA (see also AAT48239). Host recombinant alpha-7 subunit, opt. in combination with other recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunits (see also AAW09018-24, AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity.
                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.4e-97; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.7%; Score 1159.5;
ilarity 45.1%; Pred. No. 1.4e
Conservative 82; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 73-74; 108pp; English.
                                                                                                                                                                                                                        (SIBI-) SIBIA NEUROSCIENCES
                                                                                                                                                 96WO-US09775.
                                                                                                                                                                                     95US-0484722.
                                                                                                                                                                                                                                                                  Harpold MM;
ligand-gated receptor
                                                                                                                                                                                                                                                                                                     WPI; 1997-065463/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity 237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               502 AA;
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT48239
                                                                                                                                             07-JUN-1996;
                                     Homo sapiens
                                                                        WO9641876-A1
                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                  ΚЈ,
                                                                                                          27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Best Local
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Matches
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g

ROY MA;

Hillan KJ,

Gurney AL,

Goddard A,

Baker KP, Wood WI; that binds to

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proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; anglogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                          tumour; diagnosis; neoplastic disease; neoplastic cell
450 QDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                      Human PRO2145 protein sequence SEQ ID NO:77.
                                                                                                                                         Ā
                                                                                                                                   AAB24088 standard; Protein; 502
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99US-0143048.
99US-0145698.
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99WO-US12252
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99WO-US30911
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                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                     12;
                                                                                                                                 413
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                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                       68 KNQVLTTNIWLQMSWTDHYLQMNVSEYPGVKTVRFPDGQIMKPDILLYNSADERFDATFH 127
                                                                                                                                                                                                                                                      581
                                                                                                                                                                                                                                                                 245 SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 304
                                                                                                                                                                                                                                                                                                                305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR 363
                                                                                                                                                                                                                                                                                                                                                                            669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK 723
                                                                                                           67
 of
PRO\ polynucleotide and protein sequences given in the exemplification the present invention.
                                                                                                   S WILALAASLIHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDE
                                                                                                                                                                                  474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                       297 IYLNLSAK --- VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                               354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                        TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                                                           534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                              ---WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                                                    CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues
                                                                    91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; darug design; protein co-ordinate data; schizophrenia; Alzheimer's disease; nicotine addiction; Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                       CSLASVE----MSAVAPPPASNGNLLY----IGFRGLDGVHCVP-TP--
                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                  724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                              115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108.115
/note= "conserved ligand-binding region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "conserved ligand-binding region,
Trp171 and Tyr173 are essential"
210..217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trp108 and Tyr115 are essential
                                                 21;
                                                 DB
                                                Score 1159.5; DB
Pred. No. 1.4e-97
2; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotinic acetylcholine receptor alpha7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; nootropic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥Ÿ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB82690 standard; Protein; 502
                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-2001 (first entry)
                                                           al Similarity 45.1
237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171..173
                             502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                       414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB82690;
                             Sequence
                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
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                                                                   Matches
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12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Water-soluble ligand-binding proteins derived from molluscs and analogues of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 KNOLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLGDETG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||:| ::| | |:||||||||:| ||: |||| | ||:|||||:| ||:||||:|:
TNVLNNSSGHCQYLPPGIFKSSCXIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of the alpha subunit of human nicotinic acetylcholine receptor (nAChR). The sequence includes regions that are conserved throughout the various nAChR alpha subunits and which are essential for liqand binding. The invention relates to water-soluble ligand-binding proteins derived from molluscs, especially acetylcholine-binding proteins derived from malogues of ligand-gated ion channels, their crystals, and their water-soluble ligands of ligand-gated ion channels. The water-soluble ligands of ligand-gated ion channels. The water-soluble ligand-binding proteins are capable of forming multimers and are amenable to crystallization. The crystal structure of AChBP is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and thus for screening of drugs that are capable of binding a ligand of a ligand-binding domain of ligand-gated receptor, and comprise at least the amino acids of the AChBP determining solubility of the amino acids of the AChBP determining solubility of the amino acids determining binding to the ligand. In the chimeric proteins as in the AChBP and also comprising amino acids regions of an anachRP have been substituted for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 IYLNLSAK---VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
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"conserved ligand-binding region, residues
Tyr210, Cys212, Cys213 and Tyr217 are
essential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding amino acids, and preferably entire stretches have
been substituted. New drugs can be developed that selectively
intervene in neuronal signalling pathways, especially where the
ligand-gated ion channel is the nAChR, and the related disorder
Tourette's syndrome, Alzheimer's disease, addiction to nicotine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 252-254; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TEWE-) STICHTING TECH WETENSCHAPPEN.
                                                                                                                                                                                                                                                                                                                                                                             2000EP-0200443.
2000EP-0203810.
                                                                                                                                                                                                                                                                                                        09-FEB-2001; 2001WO-EP01457
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                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-497071/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sixma TK;
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Best Local Similarity
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                                                                                                                                                           WO200158951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              schizophrenia
                                                                                                                                                                                                                                                                                                                                                                             10-FEB-2000;
31-OCT-2000;
                                                                                                                                                                                                                                16-AUG-2001
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67

413 127 473 184 533 244 581

us-09-303-232-2.rag

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SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIV 304
                                                                                                                                                                                                                                                                                                                             CSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF 668
                                                                                                                                                                                                                                                                                                                                                                                                          -----DSGVV----CGRMACSPTHDEHLLHGGOPPEGDPDLAKILEEVRYIANRFRC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuronal; nicotinic acetylcholine receptor; NAChR; drug screening; hemistry; NAChR alpha7 subunit; receptor.
                                                                            -----WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                          669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                          VWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLLQIMDVDE
                                                                                                                 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                    IYLNLSAK - - - VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                    GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                        ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-------
                                                                                                                                                                                                                                                                                                                                                 and beta subunits
for in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elliott KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell comprising nucleic acids encoding human alpha and beta subunit neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans
                                                                                                                                                                                                                                                                                                                                                                                                                                   Siegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chavez-Noriega LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Examples; Page 130-131; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human neuronal NAChR alpha7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB82435 standard; Protein; 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-2001; 2001WO-US50985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claeps BO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-698532/75.
N-PSDB; ABV73248.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunochemistry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200259266-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-2003
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ABB82435
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 ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLI 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
                                      SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV
                                                                            ---WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                           305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR
                                                                                                                              CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                                                                                  669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                                                                                                                                                                                                  Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.5; DB 22; Length 502;
1.4e-97;
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                                                                                                                                              DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                  ASMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPL-
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45.1%; Pred. No. 1.4e-97;
ive 82; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; alpha7 nicotinic acetylcholine gated ion cha
5-hydroxytryptamine; 5-HT3; calcium ion conductance
                                                                                                                                                                                                                                                                                                                                                                                                            Wild-type human alpha7 ligand gated ion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Pages 61-63; 77pp; English.
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                                                                                                                                                                                                                                                                                                                             AAB50012 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2000; 2000WO-US11862.
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-061524/07.
N-PSDB; AAC90380.
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Matches 237;
185
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The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
                                                                                                                                                                                                                                                                                                                                   91;
                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                         115; Indels
                                                                                                                                                                                                                                                                                                 DB 23;
                                                                                                                                                                                                                                                                                             ; Score 1159.5; DB
; Pred. No. 1.4e-97
82; Mismatches 11:
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45.1%;
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                                                                                                                                                                                                                                                                                                                                   237; Conservative
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ion flux; alpha
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US6440681-B1

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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (nNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                             Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1159.5; DB 23;
Pred. No. 1.4e-97;
                                                                                                                                                                                                                                                                                                                      Claim 101; Column 59-64; 56pp; English.
                                                                                                                                                                         Harpold MM;
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45.1%;
                                                                   90US-0504455.
92US-0938154.
93US-0028031.
93US-0149503.
                                       95US-0487596
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Best Local Similarity 45.1
Matches 237; Conservative
                                                                                                                                            & CO INC
                                                                                                                                                                       Ellis SB,
                                                                                                                                                                                                      2002-711528/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 AA;
                                                                                                                                                                                                                  N-PSDB; ABS54875
                                                                                                                                            (MERI ) MERCK
                                                                                                               08-NOV-1993;
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                                                                                     30-NOV-1992;
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            27-AUG-2002
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This sequence is the V247r variant of human alpha7 nicotinic certytholline receptor (nAChR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 nAChR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-hereit neuralgia, diabetic neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha? NAChR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
                                                                                                                                                                                                                                                        Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 IYLNLSAK --- VCLAGYHEKRLIHDLIDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91;
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DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                  ODESEAVCSEWKFAACVVDRLCIMAFSVFTIICTIGTIGMSAPNFV 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKenna DG,
                                                                                                                                                                                                                       V274T variant human alpha7 nAChR protein
                                                                                                                    AAW69216 standard; Protein; 502 AA
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Sullivan JP, Touma
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184
                                                      TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
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TNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---
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A1292581 GH15518.5
BU9118857 AGENCOURT
AK08137 Mus muscu
AK081157 Mus muscu
CB245337 UI M-FYOBU702422 UI-M-FIO-

AK029177 Mus muscu CB149460 K-EST0205

Perfect score:

Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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BG632919 885 bp mRNA linear EST 23-APR-2001 GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. BG632919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hacapoda; Insecta; Pterygota;
Neptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophila; Drosophila.

Chases 1 to 885)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Sax: 510 486 6794
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
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BU919212
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AU120692
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AA697326
BI194994
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AK053497
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AK049722
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BX437801
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Other_ESTs: GH16126.5prime
Contact: Stapleton, M.
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EST
281.8
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228.8
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AUTHORS
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AL058211 Drosophil
AL073676 Drosophil
AL064281 Drosophil
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11127.831 Million cell updates/sec
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                                                                                        August 21, 2003, 03:48:31; Search time 5045.31 Seconds
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                                                                                                                                         US-09-303-232-1_COPY_372_2681
2310
1 atgaaaaatgcacaactgaa......caccacatattattgtctcg
                                                                                                                                                                                                                                                             45562784
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Score

. 02 Result

BX421718 BX421718 AUJ20692 AUJ20692 AK009902 MUS muscu AA697326 HL02253.5 BI194994 602944249

BX299163 BX299163

AXO53497 MUS MUSCU AKO51730 MUS MUSCU AKO80115 MUS MUSCU AKO81244 MUS MUSCU AKO49722 MUS MUSCU BK63994 170006876 BU149265 AGENCOURT BU516733 BB160023A AKO80475 MUS MUSCU BU516843 BB160023A AKO80475 MUS MUSCU BU516843 BB160023B BM711715 UT-E-CLI-AW914206 ESF345510 BW711715 UT-E-CLI-AW914206 ESF345510 BW73108 MUS MUSCU CA373069 647093 NC CB244439 UT-M-FYO-BX403124 BX403124 AL210044 Tetracadon A1110117 GH09582.5 BU195149 602944157 AKO3046 MUS MUSCU CA374163 648474 NC BU919212 6021-01 M BG404575 60242021

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more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AE0013511: arm:X [18792641,19136447] estimated-cyto:1883-1865: 04/10/2001 Plate: GH.161 row: C column: 2 High quality sequence stop: 784.
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                                                                                                                                                                                                                                                                                                                        /sex="male and female"
/dev_stage="adult"
/lab.host="bH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/clone_lib="GH"
/clone="GH"

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/mol_type="mRNA"
/db_xref="taxon:7227"
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"Web : www.genoscope.ons. France (b. Med.): Sequence was carried out as part of collaboration with the Berkeley Descepthla Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on we same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

Location/Qualifiers
                                            DNA linear GSS 03-JUN-1999 survey sequence T7 end of BAC #
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                  Drosophila melanogaster genome survey sequence T7 end of BAC # BACR02c08 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL058211 GI:4930650
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Drosophila melanogaster
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                                                                                                                                                                                                                                                                                   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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llarity 98.5%;
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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and manosate BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI disestion of Drosophila DNA provided by the BDGP from the isogenic strain v3: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                        Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK13K13 Lof RPCI-98 library from Drosophila melanogaster (fruit AL064281 Girvey sequence.
AL064281 GI:4944356
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Submitted (02-JUN-1999) Genoscope · Centre National de Sequencage :
BP 191 91006 EVRY cedex · FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 TCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGATTTGATGGCAC 295
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                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 1.9e-67;
0; Mismatches 2; Indels
                               1353 GATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGCT 1391
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                                                      425 GATGAAGTTCGGCAGTTGGACCTACGACGACGATTCCAGGT
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/db_xref="taxon:7227"
/clone="BACR13K21"
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/note="end : TET3"
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Matches 336; Conservative
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Web: www.genoscope.cns.IT.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Stitute in Buffallo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain vised for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                 CNSOOHJU 1007 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 3.1e-69;
1; Mismatches 5;
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : TET3"
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Matches 333; Conservative
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 607) | Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M. BDGP/HHMI Drosophila EST Project
                                                                     ACAGTGCGGATGAGGGATTTGACGGCACCTACCAGACGAACGTGGTGGTGCGGAACAACG
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Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AE003626: arm:2L [9617316,9882551]
estlmated-cyto:30C7-30F4: 04/10/2001
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Contact: Stapleton, M.
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// Primer. Five prime end enriched, double-strand CDNA was digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."

58 a 326 c 319 g 273 t 25 others
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                                                                                                                                                                                                                                        EST 23-MAY-2003
D Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGGTTAAAACTGGAGTGGAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCG 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1145 GAGTTAAGGATCTGCGAATACCGCCGCATCGCATCTGGAAGCCGGACGTGCTGATGTACA 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 CCCTGAGCCTCCTGCAGATCATGGACGTGGATGAGAACCAAGATCTTAACCACCAACA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCTGCACGTGTCCCTGCAAGCGAGTWCCAGAGGAAGCTTTACAAGGAGCTGGTCAAGA 229
  CTGCTAAAGTTTGCCTAGCAGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATC 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Banalis sequefefegenoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
http://www.genoscope.cns.fr
cgi-bin/cluster.gi?seq=CSODD007CH03Qpl&cluster=7646.r. Contact :
Feng Liang Email : filang@lifetech.com URL :
http://culllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD007CH03Qpl.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITATAATACACTAGAACGICCCGTICICAAIGAATCGGACCCGTTACAATTAAGCTTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTTAACTTTAATGCAAATTATCGATGTGGACGAGAAAAATCAATTGCTAGTCACTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 281.8; DB 9; Length 1201;
Pred. No. 3e-57;
5; Mismatches 322; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Feb 13, 2001 this sequence version replaced gi:12793792
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED CONA Clone CSODD007YP05 5-PRIME, mRNA sequence.
                                                                                                GATGAAGTTCGGCAGTTGGACCTACGACGACTTCCAGGT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (Dases 1 to 1201)
LI,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                       1353 GATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGCT
                                                                                                                                                                                                                                                                                                                            AL530299.2 GI:31068132
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.2%;
Best Local Similarity 59.8%;
Matches 503; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
COMMENT
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AL530299.
                                                                                                                                                                                                                                                                                                             ACCESSION
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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/db_xref="taxon:8355"
/dclone="taxon:8355"
/tissue_type="cocytes"
/lab_host="bH10B (phage-resistant)"
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/not2: Sal1; Site_1: Not1; Site_2: Sal1;
/not2: Sal1; Site_1: Not1; Site_2: Sal1; Site_1: Not1; Site_2: Sal1; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCTGCCGCCAGATTCGGGGTGAAAA 1650
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1051 GTGGACGAGAAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTGGAACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1111 ATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATACCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 TACTATTTGCAGTGGAACATGTCTGAATACCCTGGGGTAAAAATGTTCGTTTTCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1171 CATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGATTTGACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1231 ACCTACCAGACGAGCGTGGTGGTGCGGAACAACGCCTCGTGTCTATACGTTCCGCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 TCCTTTCATACTAATGTACTGGTGAACTCCAGTGGACACTGCCAATATCTGCCACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 AACCTGAAGTTTGGCTCTTGGACCTATGGTGGTCGATGGTCACTTGACCTGCAGATGCTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1471 CCCGGCAAACGTAACGAGATCTATTACAACTGCTGCCCGGAACCCTATATAGACATCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1411 GAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCGAGTGGGAACTACTGGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 TCA-----GACATATCTGAATATATCGTAAATGGAGAGTGGGACCTTGTAGGCGTT
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Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM14228 row: f column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 235.2; DB 13;
Pred. No. 5.7e-46;
0; Mismatches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 746.
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60.0%;
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                                                         Tumor Gene Index
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 415; Conserv
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ORIGIN
     AUTHORS
TITLE
                                                                                  JOURNAL
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                                                                                                             COMMENT
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                                                                                                                                                                                                       /sex="male and female"
/dev.stage="adult"
/lab_host="DH5 - alpha"
/clone_lib="GH brosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoR1; Site_2: XhoI; Sited fractionated cDNAs were directly ligated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAGAAAGCTGTCAAGGACCTCATGAAAAGCGCCTGCTGAACCATCTGCTGTCCACCTA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345
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Mphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 922)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAAGTTTGCCTAGCAGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAATACGCTGGAGCGGCCGTGGCCAATGAATCGGAGCCCCTGGAGGTTAAGTTCGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1029 AACTTTAATGCAAATTATCGATGTGGACGAGAAAAATCAATTGCTAGTCACTAATGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTAAAACTGGAGTGGAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1149 TAAGGATCTGCGAATACCGCCGCATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 CGCGGATGAGGGATTCGATGGCACGTATCACCAGCGTTGTGGTCAAACATGGCGGCAG
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IMAGE:6642638 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 140; Indels
                                                                                                  /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="GH15518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 265; DB 9;
Pred. No. 3.1e-53;
                                                                                                                                                                                                                                                                                                                                                                      Plasmid cDNA library."
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Xenopus laevis
High quality sequence stop: 521 POLYA=No.
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            162 g
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                               151 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349; Conservative
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                                                                                                                                                                                                                                                                                                Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330165116 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Isblii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwaqi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                        1651 TTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGTTTCTGAATATGGTTGCCGAG 1710
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P. and Hayashizaki, Y.
High efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                              1711 ACAATGCCGGCTACTTCCGATGCGGTGCCATT 1742
                                                                                                                                                               Mus musculus (house mouse)
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/tissue_type="diencephalon"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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RLFSGYNKWGRPVANISDVVLVRFGLSIAQLIDVDEKNOMMTTNVWVKQEWHDYKLRW
DPGDYENVTSIRIPSELIWRPDIVLYNNADGDFAVTHLTKAHLFYDGRVQWTPPAIYK
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PTGSPASLKTRPSQLPVSDQTSPCKCTCKEPSPVSPITVLKAGGTKAPPQHLPLSPAL
TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLWMFIIVCLLGTVGLFLPPW
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VTLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIRRN), Laboratory for Genome Exploration Research Group, RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, PWR:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSCSIDVIFFPFDQQNCTMKFGSWTYDKAKIDLVSMHSRVDQLDFWESGEWVIVDAVG
                                    Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2940)
                                                                                                                                                                                                                  Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Matsuyama, T., Miyazaki, A., Murata, M., Okazaki, Y., Saito, R., Saltoh, H., Sakai, C., Sakai, K., Sakacume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Taqami, M., Taqawa, A., Takahashi, F., Takaku-Akahira, S., Takaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116. 2005
/note="unnamed protein product; cholinergic receptor,
nicotinic, alpha polypeptide 4 (MCD|MGI:87888,
GB|NM_015730, evidence: BLASTN, 99%, match=1946)
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Pred. No. 3.2e-45;
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A., Shibata, K., Yoshino, M., Itch, M., Ishii, Y.,
A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
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Ia, H., Ashburner, M., Batalov, S., Casavant, T.,
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Y.T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
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J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
, Naxamura,S., Hazama,M., Nishine,T., Harada,A.,
uncto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
e.,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
wa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
atsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
sequence analysis (RISA) system-1384-format
ne with 384 multicapillary sequencer
1), 1757-1771 (2000)
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M., Hanagaki,T., Hara,A., Hashizume,W.,
M., Haramoto,K., Hiraoka,T., Hirozane,T.,
K., Ishi,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Kojima,Y., Winazaki,R., Murata,M.,
I.K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
K., Shibata,K., Shipaqawa,A., Takahashi,F., Takaku,Akahira,S.,
Tomaru,A., Toya,T., Yasunishi,A.,
                                                                                                                                                                                                                         A,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Skazaki,Y., Muramatsu,M. and Hayashizaki,Y. Ibtraction of cap-trapper-selected cDNAs to cDNA libraries for rapid discovery of new genes 1617-1630 (2000)
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h cDNAs
(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and the RIKEN Genome Exploration Research
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.-length cDNA cloning
19-44 (1999)
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UI-WFYO-cds-b-06-0-UI.rl NIH_BMAP_FYO Mus musculus cDNA clone CB245337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGTTTCTGAATATGGTTGCCG 1708
                                                                                                                                              1349 GCGAGATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGCTGGATTTACAATTACAAG 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862 AGGTCACGCTGTGCATCTCGTGCTTTCTCACCGTCTTCCTGCTGCTCATCACCG 921
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http://lmage.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
445 TCACCCACCTAACCAAAGCCCACCTGTTCTATGATGGGCGTGTGCAGTGGACACCCCCGG 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 833)
                                                1289 GGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCCCCTTCGATGACCAGCGGT
                                                                                                                                                                         GTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCTGCCGCCAGATTCGGGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        802 GCCTGCTCATCTCCTGCCTCACCGTGCTGGTCTTCTATCTGCCCTCGGAGTGCGGCGAGA
                                                                                             505 CCATCTATAAGAGCTCCTGCAGCATCGACGTCACCTTCTTCCCCTTCGACCAGCAGCT
                                                                                                                                                                                                                                              1409 ATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCGAGTGGGAACTACTGGGTG
                                                                                                                                                                                                                                                                                            622 TGCACAGCCGTGTGGACCAACTGGACTTCTGGGAAAGTGGGGAGTGGGTCATTGTGGATG
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH108 (T1 phage resistant)"
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/strain="C57BL/6"
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TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSECGEK
VTLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNVH
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EPGILGDICNQGLSPAPTFCNRMDTAVETQPTCRSPSHKVPDLKTSEVEKASPCPSPG
SCHPPNSSGAPVLIKARSLSVQHVPSSQEAAEGSIRCRSRSIQYCVSQDGAASLTESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTGSPASLKTRPSQLPVSDQTSPCKCTCKEPSPVSPITVLKAGGTKAPPQHLPLSPAL
TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLWWFIIVCLLGTVGLFLPPW
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DPGDYENVTSIRIPSELIWRPDIVLYNNADGDFAVTHLTKAHLFYDGRVQWTPPAIYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="hippocampus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
36. 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MEIGGSGAPPPLLLLPLLLLGTGLLPASSHIETRAHAEERLLK
  RIKEN Yokohama Institute; 1–7–22 Suehiro-cho, Tsurumi-ku, Yokohama,
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                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 TAGCCAATATCTCAGATGTGGTCCTTGTCCGCTTTGGCTTGTCGATTGCTCAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="unnamed protein product; cholinergic receptor, nicotinic, alpha polypeptide 4 (MGD|MGI:87888, GB|NM_015730, evidence: BLASIN, 99%, match=1946)
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                      Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 232.6; DB 11; Length 3230; Pred. No. 3.3e-45;
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                                                                                                                                                                                                                     Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="FANTOM_DB:C630019M18"
/db_xref="taxon:10090"
/clone="C630019M18"
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/db_xref="G1:26350297"
                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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illarity 56.6%;
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/clone_lib="NIH_BMAP_FYO"

/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I: The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with Oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACA. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator.

71 a 257 c 199 g 203 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATACCGCCGCATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGA 1221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGCTGGATTTACAA 1401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.9%; Score 228.8; DI Best Local Similarity 57.5%; Pred. No. 2e-44 Matches 429; Conservative 0; Mismatches 3
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/uridians="Mus musculus"
/mol.type="mknA"
/strain="C57BL/6"
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/db_xxef="taxon:10090"
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/clone_lib="NIH_BMAP_FIO"
/note="Organ: Brain; Vector: pYx- Asc; Site_1: EcoR I;
/clone_lib="NIH_BMAP_FIO"
/note="Organ: Brain; Vector: pYx- Asc; Site_1: EcoR I;
/clone_lib="NIH_BMAP_FIO"
/note="Organ: Brain; Vector: pYx- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pYx- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/note="Organ: Brain vector: pyx- Asc; Site_1: EcoR I;
/note="Organ: Brain and Not Is site and then cloned directionally into pYx-Asc vector: The library tag sequence located between the Not I site and the polya tail is CACCACGAC. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                           BUJ02422 T12-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone IMAGE: 6400763 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, Goracs, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
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                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 755)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3.3e-42;
); Mismatches 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
Contact: Robert Strausberg, Ph.D.
ATCNACGAGATCATCNCGTCCACCTC 743
                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               program coordinator.
225 c 188 g
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Location/Qualifiers
                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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BU702422.1 GI:23627209
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Best Local Similarity
Matches 412; Conserv
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DEFINITION
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ORIGIN
                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                     ACCESSION
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KEYWORDS
SOURCE
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1102 TGGAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGA 1161

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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Komno, H., Adachi, J., Fukuda, S., Aizawa, M., Nishi, K., Kiyoswa, H.; Kondo, S., Yamanaka, I., Saito, T., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochlwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washlo, T., Sakai, K., Okido, T., Fuuno, M., Aono, H., Baldarelli, R., Barshi, G., Bake, J., Boffelli, D., Bolinga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, M. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Wang, K.H., Weltz, C., Williang, L., Toyo-oka, K., Wang, K.H., Weltz, C., Williang, L., Kawaji, H., Kohtsuki, S.
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachl, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizune, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hirozane, T., Hirozane, T., Hirozane, T., Hirozane, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kothh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kokatoh, H., Kurihara, C., Matsuyama, T., Miyazaki, A., Ohno, M., Okazaki, Y., Saito, R., Saltoh, H., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4290)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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/strain="657BL/63"
/db_xref="FaNTOM_DB:4831406G09"
/db_xref="taxon:10090"
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URL:http://fantom.gsc.riken.go.jp/
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Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4831406G09 product:cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle), full insert sequence.
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                                                                                               ATACCGCCGCATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGA 1221
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        CCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCCCCTTCGATGAC
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/cell_line="CK-KI"
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/lab_host-"ToplOF""
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/note="Organ: Liver; Vector: pCNS-D2; Site_l: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The
                                                                                                                                                                                                                                                                                                                                                                                                                                      CB149460 615 bp mRNA linear EST 29-JAN-2003 K-EST0205995 L15CKK1 Homo sapiens CDNA clone L15CKK1-50-D08 5',
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 615)
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2 (boy.X.J. Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.
Oh,K.J., Cheong,J.E., Sohn,H.Y.; Kim,J.M., Park,H.S., Kim,S. and.
Kim,Y.S.
1624 ACCCTGCCGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTG
                                                                                                                                                                                                 1684 ACCGTGTTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG
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Email: 90ngsung@mail.kribb.re.kr
Plate: 50 row: D column: 08
High quality sequence stop: 615.
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/brotein_id="BAC26337.1"
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SEN WRRDVVLKNNAGOFRATIVRFTKVLLDYTGHTHTWPPPATEYSKYCEITJTHFPFDEQ
NCSMKLGTWYTDGSVVAINPESDQPDLSHPRESGEWYTKBARGWKHWYPSCCPTTPY
LDITYHFVWQRLPLYFIVNVIIPCLLFSFLTSLVFYLPDSGEKMTLSISVLLSLTVF
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                                                                                                                       /note="unnamed protein product; cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (MGD|MGI:87885, GB|NM_007389, evidence: BLASTN, 99%, match=1763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GACTACAGCAGTGTAGTCCGGCCAGTGGAGGACCACCGTGAGATTGTACAAGTCACCGTG
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Mus musculus 0 day neonate syeball CDNA, RIKEN full-length enriched library, clone:El30103El4 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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                                                                                                           1263 CGGCTCGTGTCTATACGTTCCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCAC 1322
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                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                   CGATATTGCTGATAAACGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTC
                                                                                                                             GTGGTTCCCCTTCGATGACCAGCGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGG
                                                                                                                                                                                           ATTCCAGCTGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCT
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matches 185;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
Pred No. 1.3e
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
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Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Tomita, M.,
Wagner, I., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
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Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyo-oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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AK051730 2916 bp mRNA linear HTC 05-DEC-2002 Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN FUIL-length enriched library, clone:0130068406 product:WEURONAL NICCTINIC. ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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894 GACGCTCTGCATCTCCGTGCTCCTCCTGACGGTCTTTCTCCTCGTGATCACCGAGAC 953
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                                                                             CGCCATCATCATCCGCCGACGAACACTGTACTATTCTTCAACCTGATCATACCTTGTGT
                                                                                                             1593 ACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCTGCCGCCAGATTCGGGTGAAAATT
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PFDYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEIKYNCC
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LITVELLYTTETIPSTSLYIPLIGBYLLFYMIVOLISIVITVEVLNUHHYRTPTHTHMPT
WYKAVFLILLPRVMFMTRPTSTEEDAPKTRNFYGAELSNLNCFSRADSKSCKEGYPCQ
DGTCGYCHHRRVKLSPNFSAHLTRSSSSESVDAVLSLSGALSPEIKEALQSVKYIAENMK
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/db_xref="FANTOM_DB:E130103E14"
/db_xref="taxon:10090"
/clone="E130103E14"
/tissue_type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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                           Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Stoch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Watz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stge="12 days embryo"
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MRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYF
PFDYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEIKYNCC
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LIVPELVITETIPSTSGLYPLIGETLLETMIRYTSTYGELSIVTVRYLNWHYRTPTHHWPT
WKRAPLILLETWHENTRFTSFEEDAPKTRFYGAELSINLNCFSRADSKSCKEGYPCO
DGTCGYCHHRRVKISNFSANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIABENK
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/db_xref="G1:26342156"
/translation="MGVVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFEDYNEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length corns.

Nature 420, 563-573 (2002)

( Dases I to 2916)
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                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
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URL.http://fantom.gsc.riken.go.jp/.
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/db_xref="taxon:10090"
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Direct Submission
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/strain="C57BL/6J"
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                   This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, lits regulatory regions, and antibodies directed against (1) encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AchR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster.
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                                        encoding a nicotinic acetylcholine receptor identify potential insecticides
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                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0156-ABL30511), expressed DNA sequences (ABL016176-ABL30511), expressed DNA
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                                                           GTTGACAGACTGTGCCTTATCATTCACAATGTTCGCAATATTAGCCACAATAGCTGTA
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                                                                                                                AACGTACTAGACATCGATGATGACTTCCGGCACAATTGTCGCCCCATGACGCCCGGCGGA
                                                                                                                                                                                                                      ATTGGGCCCAATTGGCAGCACCCGAATGCCGGTCACCCATCATACGTGCATCAAA
                                                                                                                                                                                                                                                                       TCATCAACTGAATATGAATTAGGTTTAATCTTAAAGGAAATTCGCTTTATAACTGATCAG
                                                                                                                                                                                                                                                                                                                          CTACGTAAAGATGACGAGTGCAATGACATTGCCAATGGAAATTTGCAGCTATGGTC
                                                                                                                                                                   <u> ACACTGCCACACAACCCGGCTTTCTATCGCACGGTTTATGGACAAGGCGACGATGGCAGC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide,
pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r detecting 7 signalling a
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2000US-0614150
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genes from Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL27131 standard;
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11-JUL-2000;
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Db 781 GCGCAACTGAGGAGCAGCAGCAGCAGCAACAGCAGCAACAGCGGCAACAGCAG	Oy 121 AACCAGAGGCACAACCAGCAACTCACAACCAAGCAAGGAGCTTAAGTACAAAACAC 180
. 838	1121
	Oy 181 CACAGCAACATTGCAAGCGAGCAGCAGCAACAGGAGCCAGCATGGAAGGAC 240
Qy 898 AAITTATCIGCIAAAGITIGC 918	1181 CACAGCAACATTGCAAGCGAGCAGCACAATAGCCAGCAACAAGGGGCAGCATCGAAGGAG
Db 901 AATTATCFGCTAAAGCAAGC 921	Qy 24.1 GAGGATGTAGCCAACCAGGTAGAAGCAATGACCAGCAGCAGCATCTGCAACAGCTAGAC 300
RESULT 3	101 BACTBACTBATTTTTTTTTTTTTTTTTTTTTTTTTTTTT
+ at.	1301 ACCAGCAACATGTTGTCGCCAAAGACAGCCCCAGCAACTGCTGCCGGCGATGAAGCA
AC ABL27130;	361 POPACCGARANCAACATAAGACTGTGTGCACGCAAGCGACAACGATTGCGTCGC
XX XX (first entry)	1361 ACAACCCAACAACAACAACATAAGACTGTGTGCACGCAAGGAAACGATGCGTCGC
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32863.	421
Drosophila; developmental biology; cell signalling; insecticide; KW pharmaceutical; gene; ds.	
XX OS Drosophila melanogaster.	Qy 464 463
AA WO200171042-A2.	Db 1481 ATCATATTAACTAAATATAGAAATTTAGAAAATAATGCACCCTCAGCACTTGAATT 1540
AA PD 27-SEP-2001.	Qy 464AGAAACAACAGCAACTIAGCATGCCTCCCTTCAAAACGCGCA 505
AA PF 23-MAR-2001; 2001WO-US09231.	Db 1541 IGGTCTTCTTACAATTGCAGAAACAACAGCAACTTAGCATGCCTCCCTTCAAAACGGCGA 1600
XX 23-WAR-2000; 2000US-191637P. PR 11-JUL-2000; 2000US-0614150.	
XX PA (PEKE) PE CORP NY.	1601 AATCCACGGACACCTACAGCACCACCAGCAATAACCAGCTGTCCGACAGCAACTACA
XX PI Venter JC, Adams M, Li PWD, Myers EW;	OY 300 TECANTICTURACURACURACIANTICANTICTURAL CONTRACTOR STANDARD TO THE TELEFORM TO THE TELEFO
AA DR WPI; 2001-656860/75. **	CAST TO TO TO THE TOTAL OF THE
New isolated nucleic acid detection reagent for detecting 1000 or more PT genes from Drosophila and for elucidating cell signalling and cell-cell	1721 CCACGCCACATTCGCCTGGGTGTTGCATGTGCTGCAGGTGCTCGTGTGCTGCAGGTGCAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGAG
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The invention relates to an isolated nucleic acid detection reagent	1781 AGTGGCAACTTCACGTGCAACAGCGATCGGTGCTACTGTTCAGAAĢGATCGCAGCGAGCA
	Oy 746 CCATCGCCTTCTATTTTAGGAGCTTTGCGGCGAGCGCAAATGCAAC 8 80.2
CC insecticides, therapeutics and pharmaceutical drugs. The invention CC discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA CC sequences (ABL01840-ABL16175) and the encoded proteins	Qy 803 GCAGCAGTAGCAGCAACAGCAGCAACAACAACAGCACGCAAATATTAAACGGACTTA 862
(ABB57737-ABB72072). The sequence data for this patent did not form part of	1901
<pre>CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wlpo.int/pub/published_pct_sequences. vx vx</pre>	Oy 863 ATAAACACTCATGGATATITTTATTGATATTTGAATTTATCTGCTAAAGTT 915
Query Match 33.6%; Score 776.2; DB 23; Length 3144; Best Local Similarity 89.0%; Pred. No. 5.5e-206; Matches 902; Conservative 0; Mismatches 13; Indels 98; Gaps 2;	RESULT 4 ABL07799 ID ABL07799 standard; cDNA; 803 BP.
Qy 1 ATGAAAAATGCACAACTGAAACTGAAGTTGACGATGATGATGAGGGCTGGCGCAGTA 60 	AA AC ABL07799; XX XX DT 26-WAR-2002 (first entrv)
61 AGATTAGCGCACTGCAGCAGCAACTTTAGCAGCAGTAGCAGCACAAAAACCACCAGCAGC	ophila melanogas
	XX KW Drosophila; developmental biology; cell signalling; insecticide; KW pharmaceutical; gene; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel nucleic acid (NA) encoding a nicotinic
                                                          CTGATTGCCTCCATGCCCTTGCTCGGATTCACCCTGCCGCCAGATTCGGGTGAAAATTA
                                                                                                                                          GCCATCATCATCCGCCGACGAACACTGTACTATTTCTTCAACCTGATCATACCTTGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. virescens acetyl-choline receptor DNA from clone Hva7-1.
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                                                                                                                                                                                                                                                                               1714 ATGCCGGCTACTTCCGATGCGGTGCCATTGTGGATAC 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "acetyl-choline receptor"
                                                                                                                                                                                                                                                                                                         AAZ24476 standard; cDNA to mRNA; 3700 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000~\mathrm{or} more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATACCGCCGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACGAGAAAAATCAATTGCTAGTCACTAATGTGTGTTAAAACTGGAGTGGAACGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 17879; 21pp + Sequence Listing; English.
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Pred. No. 9.2e-138;
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88.4%;
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 88.45
Matches 616; Conservative
                  Drosophila melanogaster
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                        pharmaceutical; gene; ss.
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                                              CCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTAATGCAAATT
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                                    GGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTATAATACACTAGAACGT
                   Gaps
Length 3700;
                  Indels
 DB 21;
                  502;
         Pred. No. 2.6e-132
                  Mismatches
Score 512.8;
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22.2%;
62.5%;
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1618 2166 2286 13 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins or more CCACACAACCCGGCTTTCTATCGCACGGTTTATGGACAAGGCGACGATGGCAGCATTGGG CTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCAGCCGCAATGCTGCCGATAC 2047 CCAATTGGCAGCACCCGAATGCCGGATGCGGTCACCATCATACGTGCATCAAATCATCA AAGGACGACGAAGATGCGGACATTTCGCGCGACTGGAAGTTCGCCGCCATGGTCGTGGAC AGACTGTGCCTTATCATATTCACAATGTTCGCAATATTAGCCACAATAGCTGTACTACTA AAAGAIGACGAGIGCAAIGACAIIGCCAAIGAIIGGAAAIIIGCAGCIAIGGICGIIGAC 2107 ACTGAATATGAATTAGGTTTAATCTTAAAGGAAATTCGCTTTATAACTGATCAGCTACGT NO 35681 developmental biology; cell signalling; insecticide; detection reagent for detecting 1000 for elucidating cell signalling and ID NO 35681; 21pp + Sequence Listing; English. ü polynucleotide

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                   Length 936;
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                                            Sequence 936 BP; 238 A; 213 C; 239 G; 246 T; 0 other;
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                                                                Score 479; DB 23;
Pred. No. 3.5e-123;
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                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell:cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 16175
                                                               developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-0614150.
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protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL07798 standard; cDNA; 14668 BP
                                                                                             17.8%;
68.8%;
                                                                                                                   Matches 565; Conservative
                                                                                                          Similarity
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                                                                                                                                                                                                              1565 ATTTCTTCAACCTGATCATACCTTGTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCA 1624
                                                                                                                                                                                                                                                        CCCTGCCGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGA 1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant
                                          GTGTCTATACGTTCCGCCGGGGATCTTCAAGTCCACGTGCAAGATCGACATCACGTT
                                                                                     GCTGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGG
                                                                                                CGAGTGGGAACTACTGGGT----GTGCCCGGCAAACGTAACGAGATCTATTACAACTGCT
                      466 TIGICIGIACGIGCCCCCTGGTAICITCAAGAGCACATGCAAGAIAGACATCACGTGGTT
                                                                                                                                                                                                                                                                                                CCGTGTTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCC 1739
                                                                                                                                                                                                                                                                                                          acid encoding a nicotinic acetylcholine receptor from ed to identify potential insecticides \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         nicotinic; insect; insecticide; scree protection agent; conductance; AChR;
                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA from clone Hva7-2.
                                                                                                                                                                                                                                                                                                                                                                        BP
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P-PSDB; AAY50816.
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                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                        AGGTCCTCACGAGAAGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCG
                                                                                                                                                                    TCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTAATGCAAAT
                                                                                                                                                                                         1044 TATCGATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTG
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Sequence 3109 BP; 923 A; 610 C; 742 G; 834 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCCGAGACCCTGCCACGGTCTCCGACGCTATCCCCCTGT
                                  DB 21;
                                 Score 411.4; DB 21;
Pred. No. 5.3e-104;
0; Mismatches 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATACCGCCGCA 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTGGAACGACAT
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                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 17876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 14668;
                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                Li PWD,
                                                                                                                                                                                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 3.7.1 les 337; Conservative
                                                                                                  pharmaceutical; gene; ss
                                                                                                                             Drosophila melanogaster.
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P-PSDB; ABB63695
                                                                                                                                                         WO200171042-A2
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO1005, PRO1141, PRO6199, PRO6190, PRO6190, PRO6190, PRO1005, PRO100
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1300 GATGAAGTTCGGCAGTTGGACCTACGACGATTCCAGGT 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO2145 nucleotide sequence SEQ ID NO:76.
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                                                                                                                                                                                                                                                                                AAC58395 standard; cDNA; 1509
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99WO-US30911.
2000WO-US00219.
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Wild-type human alpha7 ligand gated
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PRO polynuclectide and protein sequences given in the exemplification
the present invention.
                                                                                                                                                                                                                      AAGTTTGCCTAGCAGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTATA
                                                                                                                                                                                                                                                  ACGTGTCCCTGCAAGGCGAGTTCCAGAGGTTTACAAGGAGCTGGTCAAGAACTACA
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                                                                                         Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;
                                                                                                                                                                            0; Mismatches 318;
                                                                                                                      Score 296.2; DB 2
                                                                                                                                12.8%; 60.7%;
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Matches 506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the coding sequence for wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC903082 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells.
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    channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;
Human; alpha7 nicotinic acetylcholine gated ion chann
5-hydroxytryptamine; 5-HT3; calcium ion conductance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 296.2; DB 22;
Pred. No. 5.8e-72;
0; Mismatches 318;
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ilarity 60.7%;
Conservative
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P-PSDB; AAB50012.
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nes 506; Conserv
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              Nach Subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;
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immunochemistry; NAChR alpha7 subunit; gene; ss.
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/product= "NAChR alpha? subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian occytes, carrying alpha-nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits useful for identifying cpds. that
                 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor
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 Neuronal nicotinic acetylcholine receptor alpha-7 subunit DNA
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Pred. No. 6.5e-72;
); Mismatches 318; Indels
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                                                                                                                                                                                                                          Neuronal nicotinic acetylcholine receptor; nAChR; ligand-gated receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 71-73; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modulate the activity of human nAChRs
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60.7%;
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Matches 506; Conservative
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P-PSDB; AAW09025.
                                                                                                AAT48239 standard;
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                                                                                                                                isolated nucleic acid molecule comprising a sequence of nucleotides or inhomolecules that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NaChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha? subunit
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                                              Cell comprising nucleic acids encoding human alpha and beta subunits neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans -
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                        invention relates to a suitable host cell transfected with an
                                                                                                                                                                                                                                                                                                                          Score 296.2; DB 24; Length 1876;
Pred. No. 6.5e-72;
0; Mismatches 318; Indels 9;
                                                                                                                                                                                                                                                                                                 Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;
                                                                                              Examples; Page 129-130; 143pp; English.
                                                                                                                                                                                                                                                                                                                          tch 12.8%;
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506; Conservative
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                                                                                                                                                                                         895
                                        CGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGT
                                                                                                                                                                                         836 CTGCAGATTCCGGGGAGAAGATTTCCCTGGGGATAACAGTCTTACTCTCTTTACCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human neuronal nicotinic acetylcholine receptor alpha 7 subunit cDNA
                                                                                                                                                                                                                                                            TTCTGAATATGCTGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG 1743
                                                                                                                                                                                                                                                                                       TCATECTEGTCGTCGTCGTGAGATCATGCCCGCAACATCCGATTCGGTACCATTG 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; neuronal nicotinic acetylcholine receptor; nNAChR; gene;
ion flux; alpha 7 subunit.
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                                                                                                                                                                                                                                                                                    /product= "Human nNAChR alpha 7 subunit"
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                 Mismatches 318; Indels
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

August 21, 2003, 00:04:15; Search time 8610.32 Seconds (without alignments) 10975.350 Million cell updates/sec US-09-303-232-1_COPY_372_2681
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1 atgaaaaatgcacaactgaa......caccacatattattgtctcg 2310 5777422 2888711 seqs, 20454813386 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 em_htg_inv:* em_htg_other:* Minimum DB seq length: 0 Maximum DB seq length: 200000000 em_htg_hum:* em_htg_mus:* em_htg_pln:* gb_ro:* gb_sts:* gb_sy:* em_fun:* em_hum:* gb_ba:* gb_htg:* gb_un:* gb_vi:* em_ba:* em_in:* em_mu:* em_sts:* gb_in: *
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			Neor Ephy	Neoptera; Ephydroide	Endopterygota ea; Drosophili	rygc	; Diptera dae; Dros	ptera; Brachycera; Drosophila.	Muscomorpha;
	REFERENCE AUTHORS	ORS	1 Adan	l Adamczewski,M	i,M.D.,	Scł	Schulte, T.D. and		
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                                             JP 2000023680-A/I.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroida; Drosophilidae; Drosophila.
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/09, A01K67/033, C07K14/705, C07K16/28, C12N1/21, C12N5/10,
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E58346
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Nucleic acid encoding insect actyl choline receptor subunit
Patent: JP 2000023680-A 1 25-JAN-2000;
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Db 2352 ACACTGCCACAACCCGGCTTTCTATCGCACGGTTTATGGACAAGGCGACGATGCCAGC 2411 Qy 2041 ATTGGGCCAATTGGCAGCCCGAATGCCGGATGCGGTCACCCATCATACGTGCATCAAA 2100 1	RESULT 3 AF27278 LOCUS DEFINITION DIOSOPHIA melanogaster nicotinic acetylcholine receptor Dalpha5 subunit (nackalpha-34E) mRNA, nackalpha-34E-A allele, complete cds. ACCESSION AF272778 ACCESSION AF272778 TERSION REWARDS SOURCE Drosophila melanogaster (fruit fly) ORGANISM Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilae; Drosophila. REFERENCE AUTHORS TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha6, Dalpha6 and Dalpha7, in Drosophila melanogaster identify a New And Highly Conserved Target of Adenosine Deaminase Acting on THOMAL Genetics 160 (4), 1519-1533 (2002)	REFERENCE 1 (Dases 1 to 2907) AUTHORS Grauso, M. and Sattelle, D.B. AUTHORS Grauso, M. and Sattelle, D.B. JOURNAL Submission JOURNAL University of Oxford, South Park Road, Oxford Oxl 3QX, UK Location/Qualifiers Lo
		AACCTGATACTAGE CCAGATTGCTACTTGTATTGTTTTTTTTTTTTTTTTTT

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DPLQLSFGLTLAQIIDVDEKRQLLVTRWWLKLEWNDNNLRWTSDYGGVKDLRIPPHR
IMKPDVLAYRADEGFDCTYOTNVYNNNGSCLYVPPGIFKSTCKIDITWPFFDDQR
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TTFAIIIRRRLLYFFRALIFCYLLASMALLGFTLPPDSGRKLSLGYTLLLSLTVFLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                              serine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2907
                                                                                                                                                                                                                               /note="results in phenylalanine to isoleucine substitution; compared to B allele" /replace="c"
                                                                                                                                                                                                                                                                                                                                                                                                                                             and
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/gene="nAckalpha-34E"
/note="results in deletion of compared to B allele"
/replace=""
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="nAcRalpha-34E"
/note="results in asparagine
compared to B allele"
/replace="g" 634 t
                                                                                                                                                                                                                                                                                                     /note="results in threonine
compared to B allele"
/replace="t"
1079. .1080
                                                                                                                                                                        /gene="nAcRalpha-34E"
/note="compared to B allele"
/replace="a"
375
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                              1079. 1080
/gene="nAcRalpha-34E"
/note="results in lysine to
compared to B allele"
/replace="gg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="results in serine,
insertion; compared to B a
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                                                                                                                                                                                                                                                                                              /gene="nAcRalpha-34E"
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llarity 95.4%;
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AY036613.1 G. S AY036613.1 G. Drosophila me. ELNATYOCIA; Mer Rephydroidea; J. CE I (base; J. KS Grauso, M., Rev Novel Putativ, Dalpha5, Dalpi		rce	υ.	poly poly cod prod subu prod db/		SE COUNT 911 a IGIN Ouery Match Best Local Similarity Matches 2222; Conserva	1 ATGAAAATGC
DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES	gen		· .	BASE COUNT ORIGIN Query Ma Best Loc Matches	\$ d \$ d
1441 CTGAACGGGGAGTGGGAGTACTGGGTGGCCGGCAACGTAACGAGTTATTACAC 1500 1729 CTCAACGGCGAGTGGGAACTACTGGGTGGCCCGCAACGTAACGAGTTATTACAC 1500 1720 CTCAACGGCGAGTGGGAACTACTGGGTGGCCCGGCAACGTAACGAGTTATTACAC 1500 1501 TGCTGCCCGGAACCTATATAGACTTCGCCTTCGCCATCATCATCATTACAAC 1788 1501 TGCTGCCCGGAACCCTATATAGACTCACTTCGCCATCATCATCGCGAGACACT 1560 1111111111111111111111111111111111	1 CTGACCGTGTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCGCAATGCCGGCTACTTCCGATGCGGTGCCGCTACTTCCGATGCGGTGCCGTGCCAATGCCGGCTACTTCCGATGCGGTGCCAATGCCGGTGCCAATGCCGGTGCCAATGCCGGTGCCAATGCCGTTCCGATGCGGTGCCAATGCCGTTCCGATGCCGTTCCAATGCTTCATCCGATGCTTCATCCGTTGTTTATGGTAGCTTCATCCGTTGTTCCAACG	1744	1810 CTGATCCTAGAGTTCCCGACCACGCCTGTTCGGACACATCCTCCGAGCGGAAGCACCAG 1869	1930 GACATCGATGACTTCCGGCACAATGTCGCCCCATGACGCCCGGGGAACACTGCCA 1989	2050 ATTGGCAGCACCGAATGCCGGATGCGGTCACCCATCATACGTGCATCAAATCATCACT 2109	0 6 0	
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RESULT 4

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*JUDICEID__id="AAK67256.1"

//DDA.xref="G1:20340269"

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//DDA.x
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ive Nicotinic Acetylcholine Receptor Subunit Genes,
lpha6 and Dalpha7, in Drosophila melanogaster Identify a
hly Conserved Target of Adenosine Deaminase Acting on
1 A-to-1 Pre-mRNA Editing
(4), 1519-1533 (2002)
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nne="nAcRalpha34E"

tte="ion channel; neurotransmitter transmembrane

ceptor; exon 5 is excluded due to exon skipping, which

nerates a loss of reading frame and a truncated

represe illoss of reading frame and a truncated
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2834 bp mRNA linear INV 30-APR-200 elanogaster nicotinic acetylcholine receptor Dalpha5 Ralpha34E) mRNA, nAcRalpha34E-B allele, complete cds,
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dopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
to 2834)
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1_type="mRNA"
_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                    elanogaster (fruit fly)
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ap="34E4-34E5"
ev_stage="embryo"
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d Sattelle, D.B.
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	421 CGACGAAAAAGAAAACCAGCAACCCCAAACGAAACAGATATCA	10612 ATCATATTAACTAAATATATAGAAATTTAGAAAATAATTGCACCCTCAGCACTTGAATT 10671 464AGAAACAACAGCAACTTAGCAACTTGCATCCTCCAAAAACGCGCA 505		500 AATUCACGGACACCIACAGCACCAGCAGCAACAACCAGCIGICCGACAGCCACTACA 565 	566 TGCAATGTCGAGCCAGCGACAATGAGTTCAGTATTCCGATATCGAGACATGATAGAGTAT 625	626 CCACGGCCACATTCGCCTGGGTGTTGCATGTGCTGCTGCTGCTGCTGGTCGCTGCAAC 685	686 AGTGGCAACTTCACGTGCAACAGCGATCGGTGCTACTGTTCAGAAGGATCGCAGCGAGCA 745 	746 CCATCGCCTTCATTTCCTATTTAGGCAGCTTTGCAGCGCAACTGAAAAATÄGCAGCA 802 	803 GCAGCAGTAGCAGCAGCAGCAGCAACAACAGCAGCACGCAAATATTAAACGGACTTA 862 	863 ATAAACACTCAIGGATATTITATTCAIATATTIGAATTTATCIGCTAAAGTI 915 		Drosophila BACR09N24, AC092243 AC092243.1		Neopeara; Endoperaygoua; Diptera; Brachycera; Muscomotpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 158758) Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,	<pre>Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J. W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,</pre>	<pre>Fefitera,S., Filse,E., Galle,K.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Howland,T.J., Ibeywam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefl,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,</pre>	Factory, Paragos, V., Fark, S., Factory, Fitheria, Scheeler, F., Phouanenavong, S., Pithan, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Schenonia of Droscophila chromosome 2L. region 34D 34E	Unpublished 2 (bases 1 to 158758) Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., W
_	Qy Oy	oy Oy	- qa .;	Å qa	Qy Db	Qy	. Qy	Qy	. GQ	Q _y	RESULT 6 AC092243/C LOCUS	ACCESSION VERSION	SOURCE ORGANISM	REFERENCE AUTHORS			### F F	JOURNAL REFERENCE AUTHORS
	DD 2493 AAAGATGATGAATGACATTGCCAATGATTGGAAATTTGCAGCTATGGTCGTTGAC 2552 QY 2227 AGACTGTGCCTTATCATATATCACAATGTTCGCAATATTAGCCACAATAGCTGTACTACTA 2286	2613 TCAGCACCACATATATATATATATA	t omit seems to see the seeds to see the seems to see the	LOCUS ACUIVOZO 420/9 DP DNA 11DEAT HTG 10-DEC-1999 DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***. ACCESSION AC017620 1 GT-6554377	S ISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophildae; Drosophila; Losophila; Losop	Addms, M. and Venter,J.C. Direct Submissor,Bore 1999) Celera Genomics, 45 West Gude Dri Rockville, MD, USA	his sequence was identified as CDM:10211513 or more information on this record e-mail t NOTE: This is a 'working draft' sequence. This sequence will be replaced	* by the Inflance as Soon as It is available and * the accession number will be preserved. * Location/Qualifiers 1. 42079 Arranteme"hrosophila malanomaster"	/mol_type="genomic DNA" /mol_type="genomic DNA" /db_xref="taxon:7227" ORIGIN	Query Match 33 6%; Score 776.2; DB 2; Length 42079; Best Local Similarity 89.0%; Pred. No. 2.5e-201; Matches 902; Conservative 0; Mismatches 13; Indels 98; Gaps 2;	Qy 1 ATGAAAATGCACAACTGAAACTGACTGAAGTTGACGATGATGAGGTGGGCTGGCAGTA 60 	OY 61 AGATTAGCGCACTGCAGCAGCACTTAGCAGCAGCAGCACACAGAGAACCACCAGCAGC 120	OY 121 AACCAGAGGCACAACCAGCAACTCCCACACGAACCAAGGAGTTAAGTACAAAACAC 180 	Qy 181 CACAGCAACATGCAAGCAGCACAACAAGAGCAGCAACAGCAGCATCGAAGGAC 240 Db 10312 CACAGCAACATTGCAAGCAGCACAATAGCCAGCAACAGGAGCCAGCATCGAAGGAC 10371	OY 241 GAGGATGTAGCCAACCACGGTAGAAGCAATGACCAGCAGCAGCTCGCAACACTAGAC 300	QY 301 AGCAGCAACATGTTGTCGCCAAAGACAGCAGCAGCAGCAACTGCTGCCGGGGATGAAGCA 360	Oy 361 ACAACCCAACAACAACATAAGACTGTGTGCACGCAAGCGACAGCGTTGCGTCGC 420 .

0y 421 CGACGADAAAGCAGCAACCCCAAACGAACAGATATCA	566 14170 626 14110 686 14050 746 13990 803	Qy 863 ATAAACACTCATGGATATTTTATTGATATTATCTGATTATTCTGCTAAAGTT 915	AUTHORS Celliker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., AUTHORS Celliker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Rogers, Y., An, H., Baldwin, D., Banzon, J., Manantidees, P.G., Brandon, R.C., Rogers, M., Center, C., Change, M., Davenport, L.B., Dietz, S.M., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Carlson, J.W., Center, A., Change, M., Cornee, R., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., NeIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Phouanenavong, S., Pittman, G.S., Puti, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Jobases 1 to 186803) AUTHORS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., An.H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M., Dodon,K., Docrsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Inequam,C., Jalali,M., Kruse,D., Li,P., Match,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nuncoo,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Stoheeler,F., Stapleton,M., Strong,R., Svirskas,R., and Venter,J.C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C., Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS 5000RNAL Submitted (30-JUN-2001) Berkeley National Laboratory, One Cyclotron Road,	m a whole hboring c ing its l ur sequent) or sene	DASE COUNT 46829 a 33642 c 32686 g 45601 t ORIGIN QUERY'MATCH 33.6%; Score 776.2; DB 3; Length 158758; Best Local Similarity 89.0%; Pred. No. 3.3e-201; MATCHES 902; Conservative 0; Mismatches 13; Indels 98; Gaps 2; Qy 1 ATGAAAATGCACAACTGAAACTGAAGTTGACGATGATGACGTGGCTGCTGGCTG	14710 AACAAGAGGCACAACTCACAACACTCGAACCAAGGAGCTTAAGTACAAACACAACACAACACAACACAACAACAACAACAACA

625

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Drosophila melanogaster (fruit fly)

Enkaryota: Metazoa; Arthropoda; Hexapoda; Insecta: Pterygota:

Bukaryota: Metazoa; Arthropoda; Hexapoda; Insecta: Pterygota:

Bukaryota: Metazoa; Arthropoda; Hexapoda; Insecta: Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Sa Adams, M. D., Celniker, S. E., Li, P. W., Hoskins, R. A., Galle, R. F., Amanatides, P. G., Scherer, S. E., Li, P. W., Hoskins, R. A., Galle, R. F., Sutton, G. G., Wortman, J. R., Yandell, M. D., Zhang, Q., Chen, L. X., Bronden, R. C., Rogers, Y. H., Blazej, R. G., Champe, M., Pfelifer, B. D., Brandon, R. C., Baxter, E. G., Helt, G., Nelson, C. R., Gabor, G. L., Abril, J. F., Agbyani, A., An, H. J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R. M. Basu, A., Baxendale, J., Bayraktaroglu, L., Boushakov, S., Beeson, K. Y., Benos, P. V., Berman, B. P., Bhandari, D., Bolshakov, S., Berman, B. P., Bhandari, D., Bolshakov, S., Chandra, I., Cherry, J. M., Cawley, S., Dahlke, C., Davenport, L. B., Davies, P., de Pablos, B. Delcher, A., Dengar, Rocha, S., Dunkov, B. C., Dunn, P., Durbin, K. J., Evangelista, C. C., Ferraz, C., Ducka, S., Candol, C., Gabriellan, A., B., Galbar, C., Gabriellan, A., Gang, P., Harris, M. K., Gong, F., Gorrell, J. H., Gu, Z., Guan, P., Harris, M. L., Harvey, D., Heiman, T. J., Gu, Z., Guan, P., Harris, M. L., Harvey, D., Heiman, T. J.,
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                                                                                                      159760 ATCATATTTAACTAAATATATAGAAATTTAGAAAATAATTGCACCCTCAGCACTTGAATT
                                                                                                                                                                                                                                     506 AATCCACGGACACCTACAGCACCAGCAGCAACAACCAGCTGTCCGACAGCCACCTACA
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Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresenek, D., Farfan, D., Farriera, S., Frise, E., Galle, R.E., Garg, N. S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Hoskins, R.A., Hostin, D., Howland, T.J., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Phouanenavong, S., Pittman, G.S., Patel, S., Pfeiffer, B., Roshon, S., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Direct Submission

AL Submitted (39-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our send email to bdgp@fruittly.berkeley.edu.
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Matches 902;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECVPDCSASSPDNCRNGFCRSPGVČECFAEFVRNEHGACIHTCPIACQHGRCYINGTC
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Buans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y.,

Buaron, J., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,

Feriters, S., Frise, E., Galle, R.F., Gargy, N.S., George, R.A.,

Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,

McIncoh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,

Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D.,

Willams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M.

Sequencing of Drosophila melanogaster genome
Wel,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke.Z.,
Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
Kravitz,S., Kulp,D., Laliz, L., Lash,Y., Lei,Y., Lei,Y., LeriskyA.A.,
Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C.,
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Muzny,D.M., Noshrefi,A., Mounts,S.M., Moy,M., Murphy,B., Murphy,L.,
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Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden Kiamos,I.,
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The genome sequence of Drosophila melanogaster
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Submitted (23-JAN-2003) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
On Sep 16, 2002 this sequence version replaced gi:7298121.
Location/Qualifiers
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Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 272521)
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Grey,A.D.N.J., Harris,N.L., Krommiller,B., Marshall,B.,
Millburn,G.H., Richter,J., Russo,S., Searle,S.M.J., Smith,E.,
Shu,S., Smutniak,F., Whitfield,E.J., Ashburner,M., Gelbart,W.M.,
Rubin,G.M., Mungall,C.J. and Lewis,S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
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SM Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilade; Drosophila.

E 1 (bases 1 to 320754)

S Ashburner,M., Misra,S., Roote,J., Lewis,S.E., Blazej,R., Davis,T.,

Boyle,C., Galle,R., George,R., Harris;N., Hartzell,G., Harvey,D.,

Hong,L., Houston,K., Hoskins,R., Johnson,G., Martin,C.,

Moshfeil,A., Palazzollo,M., Reese,M.G., Spradling,A., Tsang,G.,

Wan,K., Whitelaw,K., Celniker,S. and Rubin,G.M.

An exploration of the sequence of a 2.9-Mb region of the genome of
                                                   CCACGCCCACATTCGCCTGGGTGTTGCATGTGCTGCTGCTGCTGCTGCTGCTAAC 685
                                                                                                                                                                                                   AGTGGCAACTTCACGTGCAACAGCGATCGGTGCTACTGTTCAGAAGGATCGCAGCGAGCA 104244
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Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Cieslolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,M., Moshrefi,M., Mixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
                                                                                                                              AGTGGCAACTTCACGTGCAACAGCGATCGGTGCTACTGTTCAGAAGGATCGCAGCGAGCA
                                                                                                                                                                                                                                                                              GCAGCAGTAGCAGCAACAGCAGCAACAACAGCAGCAGCACGCAAATATTAAACGGACTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FLYBASE:FBgn0028542"
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NSESGMASYNGSYGMSTONONTWAMOSYGMATANCOPHYPDA
VQPVTPPAHRVQVLDETALFINKTRSAMASGVCYKEVPTASLLRNSRDQFVGNGTTPD
                                                                                                                                                 PLGCGNGVCDERNECKCREGYSLEPETRKYCOPECKFGCSFGRCVAPPKKCACLOGYRL
AADGSCEPVCDSCENGKCTAPGHCNCNAGYLKLQGRCEPICSIPCKNGRCIGPDICEC
ASGFEWDRKSAECLPRCDLPCLNGVCVGNNQCDCKTGYVRDEHQRNICQPHCPQGCQN
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13:14:17 PST 2002"
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complement(10072. .11767)
/gene="BG:DS00180.8"
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prediction=method: 'genscan', version: '1.0; Date run: 19-Nov-98; Time: 15:48:39', score: '54.110'; match=method: 'TBLAGTX', version: '2.0a19MP-WashU [05-Feb-1998] [Build sol2.5-uitra 01:47:35 05-Feb-1998]', score: '329:0', 'desc:'Genbank: x99383:H.sapiens mRNA for RNA specific editase: CDS:148. 2253; PID:e254628;
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The annotation syntax used in this record is documented at
ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence_annotation.README.v
1.2.
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/clone="Pl DS01368 (D100), Pl DS08249 (D25), Pl DS08284
Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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                                                                                                                                                                                  Submitted (08-MAR-2000) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, MS 64-121, Berkeley,
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/strain="y; cn bw sp"
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                                                    Rubin, G.M.
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FEATURES

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Submitted (31-MAR-2003) Millar N.
University College London, Gower

    1. .1683
/organism="Drosophila
/mol_type="mRNA"

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/gene="nAcRalpha-18C"
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26. .1654
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TITLE
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    ESTIROFFEQLDPFNGLSDKOMSDYLYNESLRIEPRGCKTVPKFPRKWPHIPLKSPGI
KPRRONOTNSSSKLSNSTSSVAAAAASSTATSIATASAPSLHASSIMDAPTAAAANA
GSGTLAGEQSPCHNPHAFSVFRAVITERRNTSSWSGFPOHTAFDDONNEEVSVPAPHLP
KKPGAHVWANNNSTLASASAMDVVFSPALPEHLPPQSLPDSNPFASDTEAPHLP
VVSPRHEVMANNNSTLASASAMDVVFSPALPEHLPPQSLPDSNPFASDTEAPHGVCD
GAVPISPHVNVPMATNMEYRAVPPPLPPRKKERTESCADMAQKRQAPDAPTLPPRGGE
LSPPPIPPRLNHSTGISYLRQSHGKSKEFVGNSSLLLPNTSSIMIRRNSAIEKRAAAT
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                                                                                             Length 320754;
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                                                                                             Score 776.2; DB 3;
Pred. No. 3.9e-201;
0; Mismatches 13;
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llarity 89.0%;
Conservative 0
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Matches 902; Conserv
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CHALDNY NELECTRONAGE OF 1."

AD_XTEF="GI:29466437"

AD_XTEF="GI:29466437"

ALLDNY NSLERPWHENELPEATANGGRMLVYGLGLLIMIPACAAGPHEKRLLH

ALLDNY NSLERPWYNRSDEPLOLSFGITLMO! IDVDERNGLLITNIWLKLEWNDMNLRW

ALLDNY NSLERPWYNRSDEPLOLSFGITLMO! IDVDERNGLLITNIWLKLEWNDMNLRW

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STGKIDITWRPFDDQKCEMRFGSWYDOFGDLDLOLOGBGGDLSSFITNGEBUDLGVP

GKRNEIYYNGCPEPYIDITRARLITRKTLYYFRILYYFROULYGKYPNCIMFWVASSVVSTILVLNYH

RRNEIYYNGCPEPYIDITRYFLLYWFRLYYFROULYGKYPNCIMFWVASSVVSTILVLNYH

RRNEIYTHEMSEWITRYIFLYWLECILRAQFROGVGYEFPPPSSSSSASGERKQOLQN

VELKERSSKSLLANVLDIDDDFRCHHRCASATLPHQPTYTRHYRGGDGSVGPVGPA

GPVVDGRLHPATSHTCLTSSARYELALILKELRWITEQLKKEDETSDITRDWKFAAMV

VORLCLIIFTLFTITATLAVLESARPHFIVSGVRG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .S., Department of Pharmacology, Street, London, WClE 6BT, UNITED
                                                                                                                                                                                     DME554210 1683 bp mRNA linear INV 01-APR-200 Drosophila melanogaster mRNA for nicotinic acetylcholine receptor subunit Dalpha7 (nAcRalpha-18C gene).
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                                                    252547
                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases I to 1683)
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/product="nicotinic acetylcholine receptor subunit
Dalpha7"
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Length 1683;
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AJ554210.1 GI:29466436
nAcRalpha-18C gene; nicotinic acetylcholine receptor
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Pred. No. 6.8e-130;
); Mismatches 436;
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	AP143846 Heliothis virescens 7-1 subunit mRNA, co AF143846 AF143846.1 GI:48950		Unpublished Unpublished Unberger Schulter Submitted 51368, Ger	/note="hynacira7-1" /codon_start=1 /codon_start=1 /product="putative nicotinic acetylcholine receptor alpha 7-1 subunit" /protein_id="AAD32697.1" /db_xref="GI:4895005" /translation="MGGRARRSTHLAAPAGILLLLLCLLWPRGARCGYHEKRLLHHLLDH YNVLERPVVNESDPLQLSFGITHMOIIDVDERNQLLITNIMLKLEWNDMNLRWHTSDF GGWKDLRYDPHRLMKRDVLMYNSABGERDSTYPTNVVRNNGSCLYVPPGIRKSTCKI	DITWFPFDDQRCENKFGSNTYDGYQLDLQLQDEGGDDISSYTNGEWELIGYPGKRNE IYYNCCPEYIDITPAVVIRKTLYFFNLIAVPGVLIASMALLGFTLPPDSGEKLSLG VTILLSCTPPFLNAVABETWAPTSDAYPLGTYFNCTMFWASSVYSTILIANTHRRAD THEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPPPPDLELRERSSKSLLANVLD IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKD DEDADISRDWRFAAAVVDRLCLIIFTLIATLAVLLSAPHIMVS" 880 a 931 c 922 g 895 t 1 others
	RESULT 11 AF143846 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM REFERENCE AUTHORS TITLE	JOURNAL PUFFERENCE AUTHORS TITLE JOURNAL FEATURES SOULCE		BASE COUNT ORIGIN
1033 TTAATGCAAATTATCGATGTGGACGAGAAAATCCAATTGCTAGTTGTTGTTGTT 1 1 1 1 1 1 1 1 1	393 GATITACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCGAG	1513 CCCTATATAGACATCACCTTCGCCATCATCGCCGACGACGACGACTGTACTATTTCTTC 1572 11 1 1 1 1 1 1 1 1 1	1693 CTGAATATGGTTGCCGAGACAATGCCGGCTACCGATGGGTGCCATTGGGTGCGTGC	TTGTGCTGCCTGGATATTGCGAATGGCTCGCCCAGGACGACCGCTGATCCTAGAG	1879 GACGTTGAGGAGGCGCTCGTCGAAATCGCTGCCCAACGTACTAGACATCGAT 1938 1111111111111111111111111111111111
	o da da da da da da da da da da da da da	O O O O	% da % da	Oy Oy Ob	6 6 6 6

1445	RESULT 12 AX009612 LOCASION Sequence 3 from Patent EP0962528. AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 AX009612 BURATOTIS Heliothis virescens ELICATION Metaboods: Hetapoda: Insecta; Prerygota; Nectionidae; Heliothis. BURATOTIS Metaboods: Arthropoda: Hetapoda: Insecta; Prerygota; Nectionidae; Noctuoidae; Noctu	Ouery Match 22.2%; Score 512.8; DB 6; Length 3700; Best Local Similarity 62.5%; Pred. No. 4.1e-129; Matches 878; Conservative 0; Mismatches 502; Indels 24; Gaps 4; Oy 925 GGATATCATGAAAGAGACTGTTACACGATCTTTGGATCCTTATAATACACTAGAACGT 984
Query Match 22.24; Score 512.8; DB 3; Length 3629; Best Local Similarity 62.34; Fred. No. 4.1e-129; A; Best Local Similarity 62.34; Pred. No. 4.1e-129; A; Matches 878; Conservative 0; Mismatches 502; Indels 24; Gaps 4; Qy 925 GGATACCATGAACGACTGTTTTGGATCCTTATAATACATGAAGGT 984 1 1 1 1 1 1 1 1 1 1	1285 CCGGGGATCTTCAAGAGGCAAGATCGACATCACGTGCTTCCCTTCCATGACCAC 1286 CCGGGCATCTTCAAGAGCCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACCAC 1285 CCGGGCAGATGAAGATCGACATCACCTGGTTCCCCTTCGACGACCAC 1345 CGGTGCGAGATGAAGATCGACATCACCTGGTTCCCCTTCGACCAC 1405 CGATGCGAGATGAAGATTGGACTTATGATGGTTATCACTGGTTATCACTACACTA 1405 CAAGATGAACTGGCAGATATAGACACTTATGATGGTTATCACTGATCACACTACACTA 1405 CAAGATGAACTGGCAGATATAGACACTTGCTCAACGGCGAGTGGAATTAGACACT 1405 CAAGATGAACTGCATCACACACACACTATTTGTCACGAATGGCGAATGGGAATTAGACACT 1406 GAGTGCCCGGCAACACACACACACACACACTACTACTTGTCACCTGCAATGGCGAATGGGAATTAGACACTTGCTCACCTTGCTACTACTACTACTACTTGTCACCTGCGCACTACTACTACTACTACTACTACTACTACTACTACTACT	1867 CAGATACTCTCCGACGTTGAGCTGAAGAGCGCTCGTCGAAATGCTGCTGGCCAACGTA 1867 CAGATACTCTCCGACGTTGAGCTGAAGAGCGCTCGTCGAAATGCTGCTGGCCAACGTA 1385 CCGTGGGTGCTGCGATGTCACGGCCCGGCTCGGCGCGCGC

Oy 2047 CCAATTGGCAGCACCCGAATGCCGGAI Db 1565 TACAGGGGGGGTGAGGAATGCGCC Oy 2107 ACTGAATATGAATTAATCTTY Db 1619 GTCGACTACGAGTCTCCCTCATTCTC OY 2167 AAAGATGACGAGTGCAATGACATTCC Oy 2227 AGACTGTGCCTTATCATATTCTTCC Oy 2227 AGACTGTGCCTTATCATATTCACAATC Oy 2227 AGACTGTGCCTTATCATATTCCCCTC Oy 2287 TCGGCACCACATATTATTACCTTTACCCTC Oy 2287 TCGGCACCACATATTATTACTTTACCCTC Oy 2287 TCGGCACCACATATTATTATCTTTACCCTC Oy 2287 TCGGCACCACATATTATTATTCTTTACCCTC OY 2287 TCGGCACCACATATTATTATTCTTTACCCTC OY 2287 TCGGCACCACATATTATTATTCTTTACCTTC OY 2287 TCGGCACCACATATTATTATTCTTTACCTTC OY 2287 TCGCCACACATATTATTATTTTTCTTTACCTTC OY 1199 TCCGCGCCACACATTATTATTTTTTTCTTTTCCTTCTTTACCTTCTT	RESULT 13 E58347 LOCUS DEFINITION Nucleic acid encoding insect ACCESION E58347. GI:13019346 KEYWORDS JP 2000023680-A/2. SOURCE Heliothis virescens (tobacco ORGANISM Heliothis virescens and the staryota; Metazoca Arthropoc Neoptera; Endopterygota; Lepinochis virescens (tobacco Neoptera; Endopterygota; Lepinochis virescens (tobacco Neoptera; Endopterygota; Lepinochis virescens (tobacs) Noctuoidea; Noc	C1201/88, PC G01N33/15,G01N33/50//(C1 FT CDS Location/Qualifiers source (335). FEATURES 1. 3701 Anol_type="genomic If the property of the pr
985 CCGTTCCACGAGAGCGCTACTGCACCATTGGACCACACACA	CCGGGGATCTTCAAGTCGACGTGCAAGATCACGTGGTTCCCCTTCGATGACCAG [181
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TGTTCGCAATATTAGCCACAATAGCTGTACTA 2286
ATGCGGTCACCCATCATACGTGCATCAAATCATCA 2106
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9829,
NADJA ERASU,THOWAS SCHULTE PC
4/705,C07K16/28,C12k1/21,C12N5/10, PC
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pidoptera; Glossata; Ditrysia;
othinae; Heliothis.
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t actyl choline receptor subunit
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FPFDDOHCEMKFGSWTYDGNOLDLVINSEDGGDLSDFITNGFWYLLAMPGKKWTIYYA
CCPEPYVDITFTIQIRRTLYYFFNLIVPOYLLSSNALLGFTLPPDGGEKLTLGVTIL
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DFRHTISGSGTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLLIKELOFITARWKRADD
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                                                                                                                                                                                                                                                Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type I (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.
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                                                                                              Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-MRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                            AGACTGTGCCTTATCATATTCACAATGTTCGCAATATTAGCCACAATAGCTGTACTA
          AAAGATGACGAGTGCAATGACATTGCCAATGATTGGAAATTTGCAGCTATGGTCGTTGAC
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Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford C
                                                                                                                                                                                                                                                                                                                                                                                                                            Pterygota;
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoi
Roptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroides; Drosophilidae; Drosophila.
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                                                                                                                                                                    /gene="nAcRalpha-30D"
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1. .2023
                                                                                                                                                    TCGGCACCACATATTATTGTCTCG
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                                  AACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATA
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 1449 CGAGTGGGAACTACTGGGTGTGCCCGGCAAACGTAACGAGATCTATTACAACTGCTGCCC
                                CGAGTGGTACTTGCTTGCCATGCCGGGAAAGAAGAATACGATAGTCTACGCCTGCTGCCC
                                                                  GGAACCCTATATAGACATCACCTTCGCCATCATCATCGCCGACGAACACTGTACTATTT
                                                                                      CTTCAACCTGATCATACCTTGTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCT
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                  methionine substitution;
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/note="results in asparagine to glycine substitution;
compared to variant clone"
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/gene="nAcRalpha-30D"
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REPREMENT STATES ENORPHILAGES, Diplears; Brachycers; Muscomorpha; REPREMENT C. (1984) - 10.0792, M. Colatto, E. and Sattalla D. B. TITLE Dalpha; Depart M. Colatto, E. and Sattalla D. B. TITLE DALPHAGE AND DALPH		801 TITLITITITITITITITITITITITITITITITITITI	981 CGAGTGGTACTTGCCAGGAAAAAAAAAAAAAAAAAAAAA	1221 GTTCTCAACCTTGTAGTGGAGATTGCCCCAAGTATCTGATGCAATCCCTTGTTAGG 1280 1749 ACGCATCGTGTTTTGTGCTGGTGCCATGGATATTGCGAATGAGTCGCCTGGACGACCC 1808 1749 ACGCATCGTTTAGTGTGCTGCTGCTGCTGGATGATTGCCAATGATCGCCAAGGACGACC 1808 1281 CACCTACTTCAATTGCTATGTTCATGGTCGTCGTTGGTGGTGTTGATGGTT 1340 1809 GCTGATCCTAGAGTTCCCGACCACTGTTCGGACACACTCCTCCGAGGGAAGCAC- 1866 1341 GCTCAACTACCACCACCACGACGATTCACAGAGTGCACCTGGATCAAGTCGT 1400 1341 GCTCAACTACCACCACGACGTTCAAGAGGGCTCGTGCAAGTCGTGGATCAAGTCGTTAGAGTCGTGAAGTCGTAAGTCGTAAGTCGTGAAGTCGTAAGTCGTAAGTCCTGCAAATTCGTGAAGTCGTAACTCTCCGAAGTCGTGAAGTCGTAAGTAA	1401 TTTCTACATGCTGCCTGGATCTTGGGATGGTGGTGGCCGGGTGGCAGATTACAGG 1460 1924 GTACTACAATGCATGATGATGATCGCTGCTGCTGCAATTGTCGCCCCATGAC 1970 1924 GTACTACAATGCATGATGATGATGGATGGTGGAGCTGAATGGTCGCCCCATGAC 1970 19461 CAAAACAATACTATTAAGCAATGGCATGAAGGAGCTGAAAGGAGCGCTCCTCCAA 1520 1971 GCCGGCGGAACATGCCACAATGGCACTTTCTATGGACGGTTTATGGACAAGGCGA 2030 1971 ATCCCTGCTGGCCAATGGCAACCGACATGCGCACGCAATATGGACAATTGGCTC 1580 2031 CGATGGCAACTTGGCCAATTGGCAGCACCCGAATGCCGGATGCGGTCACCATCATAC 2090	
Neopters; Endopterygota; Dipters; Brachycers; Muscomorpha; Classes 1 to 2023) 10. (Lasses 1 to 2023) 11. (Lasses 1 to 2023) 12. (Lasses 1 to 2023) 13. Dalpha on Dalpha's, no Drosophila melanogaster Identi Waw and Highly Conserved Target of Adenosine Deaminase Acting of RAW-Hediated A-to-I Pre-mRN Editing Adenosine Deaminase Acting of RAW-Hediated A-to-I Pre-mRN Editing Adenosine Deaminase Acting of RAW-Hediated A-to-I Pre-mRN Editing Adenosine Deaminase Acting of RAW-Hediated A-to-I Pre-mRN Editing Adenosine Deaminase Acting of RAW-Hediated A-to-I Pre-mRN Editing Adenosine Deaminase Acting Of RAW-Hediated A-to-I Pre-mRN Editing Adenosine Deaminase Acting Of RAW-Hediated A-to-I Pre-mRN Editing Adenosine Deaminase Acting Office A-to-I RAW-Hediated A-to-I Representation Adenosine Deaminase Acting Office A-to-I RAW-Hediated A-to-I Raw-Hediated Raw-Hediated Raw-Hediated Raw-Hediated Raw-Hediated Raw-Hediated Raw-H		0 O O O O O O O O O O O O O O O O O O O	4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 d d d d d d d d d d d d d d d d d d d	90 AQ AQ AQ	da vo
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δò	2151	2151 AACTGATCAGCTACGTAAAGATGACGAGTGCAATGACATTGCCAATGATTGGAAATTTGC 2210
đ	1701	
Qy	2211	2211 AGCTATGGTCGTTGACAGACTGTGCGTTATCATATTCACAATGTTCGCAATATTAGCCAC 2270
qa	1761	
Qy	2271	2271 AATAGCTGTACTATCGGCACCACATATTATTGT 2306
QΩ	1821	1821 GGTTACGGTGCTCCTCCGCTCCGCACATAATCGT 1856
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